

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 04:07:05 ; Search time 2691 Seconds

(without alignments)  
7912.202 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aatatcatcattattatca.....tgttgcaggagaaaaaaa 713

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hcc.\*

9: gb\_estl.\*

10: gb\_est2.\*

11: gb\_hcc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_eston.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_man.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gssI.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	527.8	74.0	663	9 AU185777	AU185777 AU185777
C 2	268.2	37.6	800	14 CB958894	CB958894 AGENCOURT
C 3	147.6	20.7	663	28 AZ121459	AZ121459 RPCI-23-3
C 4	138.4	19.4	659	12 BI018962	BI018962 IL3-MT026

5	120	16.8	673	9	AV721179	AV721179
6	104.8	14.7	582	14	CB420818	CB420818 S3806 MA
7	76.6	10.7	363	13	BY547544	BY547544 BY536666
8	76.6	10.7	419	13	BY536666	BY536666 BY536666
9	73.8	10.4	855	12	BI107684	BI107684 602891529
10	58.6	8.2	1101	29	CNS0039G	AL063921 Drosophil
11	56	7.9	427	13	BA034399	BA034399 BX403499
12	56	7.9	759	29	CNS060XV	AL411257 T7 end of
13	55.6	7.8	996	29	CNS000FUF	AL071063 Drosophil
14	54.2	7.6	895	29	CNS060FSV	AL396821 T7 end of
15	54	7.5	1043	29	CNS0145P	AL103735 Drosophil
16	53.4	7.5	1099	13	BA456575	BA456575 BX456575
17	53.2	7.5	583	29	CNS044QG	AL274417 Tetradon
18	52.8	7.4	1029	29	CNS012GM	AL174271 Tetradon
19	52.2	7.3	1010	13	BA363969	BA363969 BX363969
20	51.8	7.3	909	13	BA391298	BA391298 BX391298
21	51.4	7.2	661	29	AG160661	AG160661 Pan trogl
22	51.2	7.2	928	29	CNS000KY	AL071865 Drosophil
23	50.2	7.0	1164	14	CF661469	CF661469 CcLL10a35
24	50	7.0	1184	29	CNS04PAP	AL300850 Tetradon
25	49.8	7.0	1182	9	AL513719	AL513719 AU513719
26	49.8	7.0	1201	13	BA443774	BA443774 BX443774
27	49.6	7.0	994	13	BA414650	BA414650 BX414650
28	49.6	7.0	1204	29	CNS016E2	AL106628 Drosophil
29	49.4	6.9	460	12	BI14616	BI14616 PFESTOaa4
30	49.4	6.9	1225	29	CNS0161D	AL106171 Drosophil
31	49.2	6.9	1201	13	BA360615	BA360615 BX360615
32	49	6.9	987	29	CNS014PQ	AL104456 Drosophil
33	48.8	6.8	1201	9	AL532464	AL532464 AL532464
34	48.6	6.8	452	13	BA446269	BA446269 BX446269
35	48.6	6.8	734	29	CNS010MP	AL099163 Drosophil
36	48.6	6.8	1201	9	AL581406	AL581406 AL581406
37	48.6	6.8	1201	13	BA355654	BA355654 BX355654
38	48.6	6.8	1201	13	BA439779	BA439779 BX439779
39	48.6	6.8	1201	13	BA446296	BA446296 BX446296
40	48.4	6.8	1101	29	CNS017KX	AL108171 Drosophil
41	48.4	6.8	1201	9	AL536104	AL536104 AL536104
42	48.2	6.8	1163	13	BA462115	BA462115 BX462115
43	48	6.7	1391	29	CG754863	CG754863 P050-2-GO
44	47.6	6.7	524	12	BM883775	BM883775 rc22f10.Y
45	47.6	6.7	527	12	BM883968	BM883968 rc24h04.Y

#### ALIGNMENTS

RESULT 1

AU185777/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AU185777 Homo sapiens 663 bp mRNA linear EST 05-JUL-2001  
cDNA clone B02302-019, mRNA sequence.

AU185777.1 GI:14623690

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 663)

Sugita, Y., Oshida, T. and Oya, Y.

Human cDNA sequencing

Unpublished (2001)

Contact: Yuji Sugita

Genex Research, Inc.

907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan

Tel: 81-44-797-2281

Fax: 81-44-797-2622

Email: syuji@genex.co.jp, URL: http://www.genex.co.jp.

Location/Qualifiers

1. .663

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/clone="B02302-019"
/cell_type="Mast cell"
/clone_lib="Homo sapiens Mast cell library (Sugita Y)"

Query Match      74.0%; Score 527.8; DB 9; Length 663;
Best Local Similarity 95.3%; Pred. No. 1.6e-92; Indels 5; Gaps 3;
Matches 573; Conservative 0; Mismatches 23;

ORIGIN
QY 2 ATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCTAATAACATTTGGGT 61
DB 597 AAATATCATCTATTATCATTAATCAATAAGTATTCTTTTATTCCTAATAAATTTGGGT 538
QY 62 TTTGGGATTTTAAATTTCAACACAGCAGATGACATTTTCTGTCACTATTATTATG 121
DB 537 TTGGGGATTTTAAATTTCAACACAGCAGATGACATTTTCTGTCACTATTATTATG 478
QY 122 TTGGTATGTGAAGCTATTGTTG-AGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 180
DB 477 TTGGTATGTGAAGCTATTGTTG-AGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 421
QY 181 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCACCAACCAACCAATCTTTTAGAAGACAG 240
DB 420 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCACCAACCAACCAATCTTTTAGAAGACAG 361
QY 241 TGTGACTCTACCAAGCTGTCAAAACACAGGCAAGGCGATAGTTAAAGGACGGATCT 300
DB 360 TG-GACTCTCTACCAAGCTGTCAAAACACAGGCAAGGCGATAGTTAAAGGACGGATCT 302
QY 301 TGACTCAAGAGGGTTAAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGTAAAGAAACAC 360
DB 301 TGACTCAAGAGGGTTAAATCTTGTGCTGAAGCCCTGGGGCAGGGGTGTAAAGAAACAC 242
QY 361 TTAGATTCAATGATTGTAAATTTAAGGCAATATACATATTAGTATTACCTTAGTGTAA 420
DB 241 TTAGATTCAATGATTGTAAATTTAAGGCAATATACATATTAGTATTACCTTAGTGTAA 182
QY 421 GTATCCCTGTCTATATACATAAAGTCAAAATTAAGTACCTGATGAGTGGCTGAC 480
DB 181 GTATCCCTGTCTATATACATAAAGTCAAAATTAAGTACCTGATGAGTGGCTGAC 122
QY 481 AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGATTTATCACTGGCTATGT 540
DB 121 AGTTCTAAATTTGGACTTTTAAATTTTAAATCAGTAACCTGATTTATCACTGGCTATGT 62
QY 541 GCTTAGATCTACAGAGATCATATATTGTTGATACAAATAAAGAAAGTGTCTCTCCC 600
DB 61 GCTTAGATCTACAGAGATCATATATTGTTGATACAAATAAAGAAAGTGTCTCTCCC 2
QY 601 T 601
DB 1 T 1

RESULT 2
CB958894
LOCUS AGENCOURT_13785021 NIH_MGC_184 Homo sapiens cdna clone
DEFINITION IMAGE:30352338 5', mRNA sequence.
ACCESSION CB958894
VERSION CB958894.1 GI:30215010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
```

```
cdna Library Preparation: CLONTECH Laboratories, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM51 row: e column: 19
High quality sequence stop: 488.
Location/Qualifiers
source 1.800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30352338"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_184"
/notes="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
Sfil (ggcgattggcc); Site_2: Sfil (ggcgctggcc);
Sfil (ggcgattggcc); and 3' adaptor sequence:
5'-CAGGCGATTTAGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGCGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match      37.6%; Score 268.2; DB 14; Length 800;
Best Local Similarity 99.9%; Pred. No. 3e-42; Indels 0; Gaps 0;
Matches 270; Conservative 0; Mismatches 3;

QY 1 AATATATCATCTATTATCATTAATCAATATGTTATTTTATTCCTAATAACATTTGGG 60
DB 251 AATATATCACTATTATCATTAATCAATATGTTATTTTATTCCTAATAACATTTGGG 310
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGAGATGACATTTTCTGTCACTATTATTAT 120
DB 311 TTTTGGGATTTTAAATTTTCAACACAGCAGAGATGACATTTTCTGTCACTATTATTAT 370
QY 121 GTTGTGATGTGAAGCTATTGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 180
DB 371 GTTGTGATGTGAAGCTATTGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA 430
QY 181 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCACCAACCAACCAATCTTTTAGAAGACAG 240
DB 431 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCACCAACCAACCAATCTTTTAGAAGACAG 490
QY 241 TGTGACTCTCTACCAAGCTGTCAAAACACACAGG 273
DB 491 TGTGACTCTCTACCAAGCTGTCAAAACACACAGG 523

RESULT 3
AZ121459/c
LOCUS AZ121459.1 TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,
DEFINITION genomic survey sequence.
ACCESSION AZ121459
VERSION AZ121459.1 GI:7788387
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 663)
Zhaoh, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
```

JOURNAL  
COMMENT

Unpublished (1999)  
Other GSSs: RPCI-23-30A15.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: shzhaotigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.bufo.edu/orderingframe.htm>) or from Resea ch Genetecs (info@resgen.com). BAC end page: [http://www.tigr.org/tdb/bac/ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html)  
Plate: 30 row: A column: 15  
Seq primer: T7  
Class: BAC ends.

FEATURES  
source

1. .663  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-30A15"  
/sex="Female"  
/lab\_host="DH10B"  
/clone\_lib="RPCI-23"  
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 20.7%; Score 147.6; DB 28; Length 663;  
Best Local Similarity 71.6%; Pred. No. 7.3e-19;  
Matches 252; Conservative 0; Mismatches 89; Indels 11; Gaps 4;  
QY 1 AATATATCATCTATTATCAATCAATCAATGATTTCT-TTATTCATCAATCAATTTGG 59  
Db 351 AACATACAGTTTATTTATCAATCAATCAATGATTTCTTTATTCATCAATTTGG 292  
QY 60 GTTTTGGGATTTTAAATTTCAACACAGCAGATGACAT-TTTTCTGTCATTTATT 117  
Db 291 GTGCTGGCATTTCCATTTTAAACACAGCAGATGATTTCTTTTCTGTCATTTGCT 232  
QY 118 ATTGTTGGTATGGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACATTTGGGAATGG 177  
Db 231 GTTCGTGACGTATCAAGCAATTTTGTGACACAAATTCAGGGAGAAATCCAGAGGAGAAAA 172  
QY 178 CTACTTTCTATCAGAAATCAAGACACAGTCAACCCACACATCTTTAGAGA 237  
Db 171 CAATCTTCTATCAAGAATAAAGAGAACCA---AGCCCCACAGAAATCATCTTTAGATGA 115  
QY 238 CAGTGTGACTCTTACCAAGCTGTCAAAACACAGGCAAGGGCATAGTTAAAGCA---- 292  
Db 114 GAAGTGTGCTCCCTCCAGGCATCCCAACTACAGGCAAGGGCAGCAGGAAGGCAAT 55  
QY 293 CGGAATCTTGACTCAAGAGGTTTAATTTCTTGGTCTGAAGCCTTGGGCGAGGG 344  
Db 54 GGGATCCCGGATTCAGAGGTTTCATTTCTTGGTCTGAGGCTGGGCTGGGCTGGG 3

RESULT 4  
BI018962/c

LOCUS BI018962  
DEFINITION IL3-MT0267-050101-437-A02 MT0267 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BI018962  
VERSION BI018962.1 GI:14425592  
KEYWORDS EST.

SOURCE  
ORGANISM

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 659)

REFERENCE  
AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL  
MEDLINE  
PUBMED

20202663

## COMMENT

10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&et2=IL3-MT0267-050101-437-A02&t3=2001-01-05&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 639.

## FEATURES

Location/Qualifiers  
source  
1. .659  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="MT0267"  
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 19.4%; Score 138.4; DB 12; Length 659;  
Best Local Similarity 99.3%; Pred. No. 4.4e-17;  
Matches 139; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 134 GCTATTGGAGATCCCAATTCAGGAAGCAACACATTCGAGATGGCTACTTTCTATCAAGA 193  
Db 572 GCTATTGGAGTCCCAATTCAGGAAGCAACACATTCGAGATGGCTACTTTCTATCAAGA 513  
QY 194 AATAAGAGAACCAAGTCAACCCACACATCATCTTTAGAGACAGTGTGACTTCCTACC 253  
Db 512 AATAAGAGAACCAAGTCAACCCACACATCATCTTTAGAGACAGTGTGACTTCCTACC 453  
QY 254 AAAGCTGTCAAAACCAAGG 273  
Db 452 AAAGCTGTCAAAACCAAGG 433

RESULT 5  
AV721179

LOCUS AV721179  
DEFINITION HTB Homo sapiens cDNA clone HTBAKFl1 5', mRNA sequence.  
ACCESSION AV721179  
VERSION AV721179.1 GI:10818331  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 673)
Gu, Y., Peng, Y., Qian, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qiu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z., and Han, Z.
Homo sapiens cDNA HTB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzge@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
    source
        1..673
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="HTBAKFl1"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /clone_lib="HTB"
            /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
            XhoI"

ORIGIN
Query Match          16.8%; Score 120; DB 9; Length 673;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 AGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACCAAGTCA 213
Db 1 AGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACCAAGTCA 60

QY 214 ACCCACAAATCATCTTTAGAGACAGTGTCACCTCCTACCAAGCTGTCAAACCCACAGG 273
Db 61 ACCCACAAATCATCTTTAGAGACAGTGTCACCTCCTACCAAGCTGTCAAACCCACAGG 120

RESULT 6
CB420818          582 bp mRNA linear EST 25-MAR-2003
LOCUS
DEFINITION
593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION
CB420818
VERSION
CB420818.1 GI:29187264
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 582)
Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E., and Keefe, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: FQY8014 row: B column: 7
Seq primer: GTAATACGATCCTACCTATAGG.

FEATURES
    source
        1..582
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            /mol_type="mRNA"
            /db_xref="taxon:9913"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /clone_lib="MARC 6BOV"
            /notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
            Library made with RNA pooled from multiple tissues
            including liver, lung, hypothalamus, pituitary, and
            placenta/endometrium."

ORIGIN
Query Match          14.7%; Score 104.8; DB 14; Length 582;
Best Local Similarity 84.3%; Pred. No. 1.5e-10;
Matches 118; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 134 GCTATTTGGAGATCCCAATTCAGGAAGCAACACATTCGGAATGGCTACTTTCTATCAAGA 193
Db 244 GGTATTTGGAGATCCCAAGTTCAGGGAACAACCTGTTGAAGAGTGACAGCTTTCCATCAAGA 303

QY 194 AATAAGAGAACCAACAGTCAACCCACCAATCATCTTTAGAGACAGTGTGACTCTTACC 253
Db 304 AATAAGAGAACCAACAGTCAACCCACCAATCATCTTTAGAGATAGTGTGATACCTTACC 363

QY 254 AAGCTGTCAAACCCACAGG 273
Db 364 AAGCTGTCAAACCCACAGG 383

RESULT 7
BY547544          363 bp mRNA linear EST 14-DEC-2002
LOCUS
DEFINITION
BY547544 RIKEN full-length enriched, B6-derived CD11 +ve dendritic
cells Mus musculus cDNA clone F73011908 3', mRNA sequence.
ACCESSION
BY547544
VERSION
BY547544.1 GI:26881923
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 363)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Buit, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, R., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
MEDLINE

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12466851  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp/  
 URL: http://genome-gsc.riken.go.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
 Trust/MRC building Addenbrookes Hospital Cambridge) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site (http://genome-gsc.riken.go.jp) for  
 further details.  
 FEATURES  
 Location/Qualifiers  
 source  
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 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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 +ve dendritic cells"

ORIGIN  
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 Best Local Similarity 69.8%; Pred. No. 5e-05;  
 Matches 132; Conservative 0; Mismatches 54; Indels 3; Gaps 2;  
 QY 1 AATATATCATCTATTATTCATTAATCAATATGATTTCT-TTTATTCCAATAAATGG 59  
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 Db 175 AACATACAGTTTATTATTCATTAATCAATATGATTTCT-TTTATTCCAATAAATGG 234  
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 QY 60 GTTTTGGGATTTTAAATTTTCAACACAGCAGATGACAT-TTTTCTGTCATTTATT 117  
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 Db 235 GTGCTGGCATTTTCAATTTTAAACACAGCAGATGACATTTTCTGTCATTTATTGCT 294  
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 QY 118 ATTGTTGGTATGTGAAGTATTTGGAGATTTTGGAGATCAATTCAGGAGCAACATTTGGAGATGG 177  
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 Db 295 GTTCGTGACGTATGAGCAATTTTGGCGACACATTTCCGGGAGAAATCCAGGAGGAAGA 354  
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 QY 178 CTACTTTCT 186  
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 Db 355 CAACTTCT 363  
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RESULT 8  
 BY536666

LOCUS  
 DEFINITION  
 BY536666 419 bp mRNA linear EST 14-DEC-2002  
 BY536666 RIKEN full-length enriched, NOD-derived CD11c +ve  
 dendritic cells Mus musculus cDNA clone F63031IP20 3', mRNA  
 sequence.  
 BY536666  
 EST  
 BY536666.1 GI:26871045  
 Mus musculus (house mouse)

ORGANISM

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SOURCE

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
source  
Location/Qualifiers  
1. 419  
/organism="Mus musculus"  
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Db 291 GTGCTGCATTTCCATTTTAAACACAGCAGAAATGACATTTCTTTTCTGTCACATTAATTGCT 350  
QY 118 ATTCTTGCTATGTGAAGTATTTGGAGATCCAAATTCAGGAGCAACATTTGGAGAAATGG 177  
Db 351 GTTCGTACGTATGAGCAATTTGGACACAAATTCAGGAGAAATTCAGGAGGAGAAAGA 410  
QY 178 CTACTTTCT 186  
Db 411 CAACTTCT 419

RESULT 9  
BI107684  
LOCUS  
DEFINITION  
602891529F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5036647 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 855)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LWA1101 row: j column: 08  
High quality sequence start: 27  
High quality sequence stop: 825.  
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Stem cell origin."  
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/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Salt;  
Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 10.4%; Score 73.8; DB 12; Length 855;  
Best Local Similarity 75.2%; Pred. No. 0.00013;  
Matches 106; Conservative 0; Mismatches 32; Indels 3; Gaps 1;  
QY 133 AGCTATTGGAGATCCCAATTCAGGAAGCAACATTTGGAGAAATGGTACTTTTATCAAG 192  
Db 310 AGCATTATGGAGACACAATTCAGGGAGAAATCCAGAAGAGAGAAACATTTCCCATCAAG 369  
QY 193 AATAAAGAGAACCAAGTCACCCACACATCATCTTTAGAGACAGTGTGACTCTCTAC 252  
Db 370 AATAAAGAGAACCAACA--AGCCACAGAAATCATCTTTAGATGAGAAAGTGGTCTCCTC 426  
QY 253 CAAAGCTGTCAAAACCAACAGG 273  
Db 427 CAAGGCATCCCAACTACAGG 447

RESULT 10  
CNS0039G/c  
LOCUS

DEFINITION  
CNS0039G 1101 bp DNA linear GSS 03-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL063921  
GI:4941778  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : [secre@genoscope.cns.fr](mailto:secre@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>  
The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoler in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
Location/Qualifiers  
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/note="end : TET3"



11152892  
 PUBMED  
 3 (Bases 1 to 759)  
 REFERENCE  
 Genoscope.  
 AUTHORS  
 Direct Submission  
 TITLE  
 Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,  
 JOURNAL  
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

## COMMENT

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

## FEATURES

source

1..759

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/clone\_lib="AW0AA"

/note="end : 77"

## ORIGIN

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Best Local Similarity 40.4%; Pred. No. 0.39;

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QY 348 TAAAGAAAACACCTTAGTTCATCATCTAAATTTAAGGCAATACACATATTAGTATT 407

Db 3 TATMAATACCCGTTAAATTTCTTTTAAATTTTAAATTTTAAATTTTAAATTTT 62

QY 408 ACCTTAGTGTATGATCCCTGCATATATACATTAAGGTGAATTAAGTAC-CCTAT 466

Db 63 AATTTATTATTATTTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTAT 122

QY 467 GCAGTTGGCTGCAGCTTCTAAATTTGAGCTTTATTTATTTTAAATTCAGTAACTGATT 526

Db 123 TTAMATTTATWTAMATTTATWTAMATTTATWTAMATTTATWTAMATTTATWTAMAT 182

QY 527 ATCACTGGCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAGTCTAG 586

Db 183 WAAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAWMAW 242

QY 587 AGTGTCTCTCCCTTACAGATTGACATTTTAAATCGCATACAGTTAGATAGGAATA 646

Db 243 AAANAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 302

QY 647 TGACATTAGAAAGGAGATGACAGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 706

Db 303 AAAAAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAAAMMAA 362

QY 707 AAAAAA 712

Db 363 AAWMA 368

## RESULT 13

CNS00FUH

LOCUS

DEFINITION CNS00FUH 996 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC:

BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION AL071063

VERSION AL071063.1 GI:4951105

KEYWORDS GSS

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (Bases 1 to 996)  
 Genoscope.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org/TheBDGP/Drosophila>  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mamoser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones the entire library or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1..996

/organism="Drosophila melanogaster"

/mol\_type="genomic DNA"

/db\_xref="taxon:7227"

/clone\_lib="RPCI-98"

/note="end : TET3"

## ORIGIN

Query Match 7.8%; Score 55.6; DB 29; Length 996;

Best Local Similarity 40.3%; Pred. No. 0.42;

Matches 128; Conservative 45; Mismatches 141; Indels 4; Gaps 1;

QY 349 AAAGAAAACACTTAGATTCAATTCATTTAAATTTAAGGCAATACACATATTAGTATTA 408

Db 538 AAAAAAATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 597

QY 409 CCTTAGTGAATGATCCCTGCATATATACATAAAGGTGAATTAAGTACCTTATGC 468

Db 598 WATTTTCWAAAATTTWAAATTTWAAATTTWAAATTTWAAATTTWAAATTTWAAATTT 657

QY 469 AGTTGGCTGGACAGTCTCAATTCGACTTTTAAATTTTAAATTCAGTAACTGATTAT 528

Db 658 WGTTTAAATMAATCAATTAATAATAATAATAATAATAATAATAATAATAATAATA 717

QY 529 CACTGGCTATGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAG 588

Db 718 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 773

QY 589 TGTTCCTCCCTTACAGAAATGACATTTTAAATCGCATACAGTTAGTAAATATG 648

Db 774 WATTTTWTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 833

QY 649 ACAATTAGAAGGAAGAT 666

Db 834 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 851

## RESULT 14

CNS06FSV

LOCUS

DEFINITION CNS06FSV 895 bp DNA linear GSS 17-JUN-2001

T7 end of clone AR0AA032H05 of library AR0AA from strain CBS 732 of

Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL396821

VERSION AL396821.1 GI:12149222

KEYWORDS GSS

SOURCE Zygosaccharomyces rouxii

ORGANISM Zygosaccharomyces rouxii

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 06:04:01 ; Search time 406 Seconds

(without alignments)  
6568.364 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aatatacatctattatca.....tggtgcaagaaaaaaa 713

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	713	100.0	713	9	US-09-989-723-376
3	713	100.0	713	9	US-09-989-279-376
4	713	100.0	713	9	US-09-989-727-376
5	713	100.0	713	9	US-09-989-731-376
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7	713	100.0	713	9	US-09-991-073-376
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9	713	100.0	713	9	US-09-991-163-376
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## ALIGNMENTS

## RESULT 1

US-09-989-722-376

; Sequence 376, Application US/09989722

; Patent No. US20020072067A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Deenoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Forgy, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C63

; CURRENT APPLICATION NUMBER: US/09/989,722

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 5e-161;
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; Sequence 376, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1G62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
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Query Match 100.0%; Score 713; DB 9; Length 713;  
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; GENERAL INFORMATION:					
; APPLICANT: Ashkenazi, Avi J.					
; APPLICANT: Baker, Kevin P.					
; APPLICANT: Botstein, David					
; APPLICANT: Desnovers, Luc					
; APPLICANT: Eaton, Dan L.					
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; APPLICANT: Tumas, Daniel					
; APPLICANT: Watanabe, Colin K.					
; APPLICANT: Williams, P. Mickey					
; APPLICANT: Wood, William I.					
; APPLICANT: Zhang, Zemin					
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
; FILE OF INVENTION: Acids Encoding the Same					
; FILE OF INVENTION: P2730PLC56					
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Best Local Similarity 100.0%; Pred No. 5e-161;
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 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
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 ; APPLICANT: Napier, Mary A.  
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 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1G57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 5e-161;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US2002012756A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C15  
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; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787

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RESULT 8  
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 ; Sequence 376, Application US/09990442  
 ; Patent No. US20020132252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Geritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: KJavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 ; FILE REFERENCE: P2730P1C8  
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 ; PRIOR FILING DATE: 1997-06-15  
 ; PRIOR APPLICATION NUMBER: 60/062250  
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56	PRIOR FILING DATE: 1998-07-07	
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Qy	121 GTTGGTATGTGAAGCTATTTTGGAGATCCAATTCAGGAAGCAACACATTGGAGATGGCTA	180





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PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 713; DB 9; Length 713;  
Best Local Similarity 100.0%; Pred. No. 5e-161;  
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DB 541 GCTTAGATCTACAGGAGATCATATAATTTTGATACAAATAAGAAAGTGTCTCTCCCC 600  
QY 601 TTACAGAAATGACATTTTAAATTCGGATACAGTTAGATAGGAATATGACATTAGAAAG 660  
DB 601 TTACAGAAATGACATTTTAAATTCGGATACAGTTAGATAGGAATATGACATTAGAAAG 660  
QY 661 AAGNATCAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713



121	QY	GTG	GTATG	TGTAAGCTATTTG	TGAGATCCAAATTCAGGAAGCAACACATTTGAGAAATGGCTA	180
121	Db	GTG	GTATG	TGTAAGCTATTTG	TGAGATCCAAATTCAGGAAGCAACACATTTGAGAAATGGCTA	180
181	QY	CTTTCTTATCAAGAAATAAAGAGAACACACAGTCAACCCACACAATATCATCTTTAGAAAGCAG	240			
181	Db	CTTTCTTATCAAGAAATAAAGAGAACACACAGTCAACCCACACAATATCATCTTTAGAAAGCAG	240			
241	QY	TGFGACTCCTTACAAAGCTGTCTAAACACACAGCGAAGGGCATAGTTTAAAGACGCGGAATCT	300			
241	Db	TGFGACTCCTTACAAAGCTGTCTAAACACACAGCGAAGGGCATAGTTTAAAGACGCGGAATCT	300			
301	QY	TGSACTCAAGAGGGGTAAATCTTCGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC	360			
301	Db	TGSACTCAAGAGGGGTAAATCTTCGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC	360			
361	QY	TTAGATTCAATGATTGTAAATTTTAAAGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420			
361	Db	TTAGATTCAATGATTGTAAATTTTAAAGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420			
421	QY	GTATCCCTGTGCATATATACAAATAAGGTGAAATTTATAAGTACCCCTATGCGAGTTGGCTGGAC	480			
421	Db	GTATCCCTGTGCATATATACAAATAAGGTGAAATTTATAAGTACCCCTATGCGAGTTGGCTGGAC	480			
481	QY	AGTTCTTAAATTTGGACTTTATTTTAAATTTTAAATCAGTAACTGATTTTATCACTGGGTATGT	540			
481	Db	AGTTCTTAAATTTGGACTTTATTTTAAATTTTAAATCAGTAACTGATTTTATCACTGGGTATGT	540			
541	QY	GCCTTAGATCTACAGGAGATCATATAATTTTGATACAAATATAAGAAAAAGTGTCTCTCCCC	600			
541	Db	GCCTTAGATCTACAGGAGATCATATAATTTTGATACAAATATAAGAAAAAGTGTCTCTCCCC	600			
601	QY	TTACAGAATTTGACATTTTAAATGGCATACAGTTTGAATAGGAATATACATTAGAAAGG	660			
601	Db	TTACAGAATTTGACATTTTAAATGGCATACAGTTTGAATAGGAATATGACATTAGAAAGG	660			
661	QY	AAGAAATGACAGGGAGAAAGGAAAGAGGGAAAAATGTTGCCAGGAAAAA	713			
661	Db	AAGAAATGACAGGGAGAAAGGAAAGAGGGAAAAATGTTGCCAGGAAAAA	713			

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RESULT 13
US-09-992-598-376
Sequence 376, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Tr
FILE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730P1C20

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PRIOR APPLICATION NUMBER: 60/090254	
PRIOR FILING DATE: 1998-06-22	
PRIOR APPLICATION NUMBER: 60/090349	
PRIOR FILING DATE: 1998-06-23	
PRIOR APPLICATION NUMBER: 60/090355	
PRIOR FILING DATE: 1998-06-23	
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PRIOR FILING DATE: 1998-06-24	
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PRIOR FILING DATE: 1998-07-01	
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PRIOR FILING DATE: 1998-07-02	
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PRIOR FILING DATE: 1998-07-01	
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PRIOR FILING DATE: 1998-07-02	
PRIOR APPLICATION NUMBER: 60/091971	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/09198	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/09218	
PRIOR FILING DATE: 1998-07-09	

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Db	1	AAATATATCATCTATTTATCATTAATCAATTAATGTATTCCTTTATTCCTCAATAACATTTGGG	60		
Qy	61	TTTTGGGATTTTAATTTTCAAACACAGCAGATACATTTTTCGTGCATTTATTATTATT	120		
Db	61	TTTTGGGATTTTAATTTTCAAACACAGCAGATACATTTTTCGTGCATTTATTATTATT	120		

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, PRIOR APPLICATION NUMBER: 60/090696
, PRIOR FILING DATE: 1998-06-25
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, PRIOR APPLICATION NUMBER: 60/090863
, PRIOR FILING DATE: 1998-06-26
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, PRIOR FILING DATE: 1998-07-01
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, PRIOR FILING DATE: 1998-07-02
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, PRIOR APPLICATION NUMBER: 60/091633
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, PRIOR APPLICATION NUMBER: 60/091788
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/091822
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/092182
, PRIOR FILING DATE: 1998-07-09

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Query Match      100.0%; Score 713; DB 9; Length 713;
Best Local Similarity 100.0%; Pred. No. 5e-161;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	AATATATCATCTTATTTATCAATTAATCAATTAATGATTTCTTTATTTCCAAATAACAATTTGGG	60
Db	1	AATATATCATCTTATTTATCAATTAATCAATTAATGATTTCTTTATTTCCAAATAACAATTTGGG	60
QY	61	TTTTGGGATTTTAAATTTTCAAAACACAGCAGAATGACATTTTCTGTCACTATTATTATT	120
Db	61	TTTTGGGATTTTAAATTTTCAAAACACAGCAGAATGACATTTTCTGTCACTATTATTATT	120
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Db	121	GTTGGTATGTGAAGCTATTTGGAGATCCAATTTAGGAAGCAACACATTTGGGAATGGCTA	180
QY	181	CTTCTCTATCAAGAAATTAAGAGAACCCAGTCAACCCACACAAATCATCTTTAGAGAGACAG	240
Db	181	CTTCTCTATCAAGAAATTAAGAGAACCCAGTCAACCCACACAAATCATCTTTAGAGAGACAG	240
QY	241	TGTGACTCTTACCAAAGCTGTCAAAACCCACAGGCAAGGCATAGTTAAAGGACGGAATCT	300
Db	241	TGTGACTCTTACCAAAGCTGTCAAAACCCACAGGCAAGGCATAGTTAAAGGACGGAATCT	300
QY	301	TGACTCAAGAGGGTTAATTTCTTGGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAACAC	360
Db	301	TGACTCAAGAGGGTTAATTTCTTGGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAACAC	360
QY	361	TTAGATTCAATGTATGTATAATTTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420
Db	361	TTAGATTCAATGTATGTATAATTTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAAT	420
QY	421	GTATCCCTGTGCATATATACAAATAAGGTGAATTAATGAATGCCATATGCAGTTGGCTGGAC	480
Db	421	GTATCCCTGTGCATATATACAAATAAGGTGAATTAATGAATGCCATATGCAGTTGGCTGGAC	480
QY	481	AGTTCTAAATTTGGACCTTTATTAATTTTAAATTCAGTAACTCATTTATTCACATGGCTATGT	540
Db	481	AGTTCTAAATTTGGACCTTTATTAATTTTAAATTCAGTAACTCATTTATTCACATGGCTATGT	540
QY	541	GCTTAGATCTCAGAGAGATCATATAATTTTGATACAAATAAAAGAAAGTGTCTCTCCCC	600
Db	541	GCTTAGATCTCAGAGAGATCATATAATTTTGATACAAATAAAAGAAAGTGTCTCTCCCC	600
QY	601	TTACAGAAATGTGACATTTTAAATTCGGGATACAGTTAGAAATAGGAATATGACATTAGAAAGG	660
Db	601	TTACAGAAATGTGACATTTTAAATTCGGGATACAGTTAGAAATAGGAATATGACATTAGAAAGG	660

QY 661 AAGAAATGACAGGGAGAAAGGGAAGAAAGGGAATAATGTTGCCAAGGAAAAA 713

Dp 661 AAGAAATGACAGGGAGAAAGGGAAGAAAGGGAATAATGTTGCCAAGGAAAAA 713

## RESULT 14

US-001-989-293A-376  
Sequence 3/76, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
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PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04

	Query Match	100.0%;	Score 713;	DB 9;	Length 713;
	Best Local Similarity	100.0%;	Pred. NO.5e-161;		
	Matches 713;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Qy	1	AATATATCATCTATTTTATCATTAATCAATATGATGATTCTTTTATTTCCAAATCAACATTGGG	60		
Db	1	AATATATCATCTATTTTATCATTAATCAATATGATGATTCTTTTATTTCCAAATCAACATTGGG	60		
Qy	61	TTTTGGCATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATT	120		
Db	61	TTTTGGCATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATT	120		

QY 121 GTTGGTATGTGAAGCTATTGGAGATCCAAATTCAGGAAGCAACACATTCGGATGGCTA 180  
Db 121 GTTGGTATGTGAAGCTATTGGAGATCCAAATTCAGGAAGCAACACATTCGGATGGCTA 180  
QY 181 CTTTCTATCAAGAAATAAAGAGAACACACAGTCACACCCACACAAATCATCTTTAGAGACAG 240  
Db 181 CTTTCTATCAAGAAATAAAGAGAACACACAGTCACACCCACACAAATCATCTTTAGAGACAG 240  
QY 241 TGTGACTCCTACCAAGCTGTCAAAACACACAGGCAAGGCATAGTTAAAGACGGAATCT 300  
Db 241 TGTGACTCCTACCAAGCTGTCAAAACACACAGGCAAGGCATAGTTAAAGACGGAATCT 300  
QY 301 TGACTCAAGAGGGTTAATCTTGTGCTGAAGCCTGGGCGAGGGTGTAAAGAAACAC 360  
Db 301 TGACTCAAGAGGGTTAATCTTGTGCTGAAGCCTGGGCGAGGGTGTAAAGAAACAC 360  
QY 361 TTAGATCAATGATGTAAATTTAAGGCAATAACATATTTAGTATTTACCTTAGTGTAAAT 420  
Db 361 TTAGATCAATGATGTAAATTTAAGGCAATAACATATTTAGTATTTACCTTAGTGTAAAT 420  
QY 421 GTATCCCTGTCATATATACATATAGGTGCAATTTAAGTACCTTATGAGTTGGCTGGAC 480  
Db 421 GTATCCCTGTCATATATACATATAGGTGCAATTTAAGTACCTTATGAGTTGGCTGGAC 480  
QY 481 AGTTCTAAATTTGGACTTTATTAATTTTAAATCAGTAACCTGATTTATCACTGGCTATGT 540  
Db 481 AGTTCTAAATTTGGACTTTATTAATTTTAAATCAGTAACCTGATTTATCACTGGCTATGT 540  
QY 541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCC 600  
Db 541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCC 600  
QY 601 TTACAGAAATTCACATTTTAAATGGATACAGTTAGATAGGATATGACATTTAGAAAGG 660  
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QY 661 AAGAAATGACAGGAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAG 713  
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## RESULT 15

US-09-989-735-376

Sequence 376, Application US/09989735

Publication No. US20020193299A1

## GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary B.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C61  
CURRENT APPLICATION NUMBER: US/09/989, 735  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11



/	PRIOR FILING DATE:	1998-06-25
/	PRIOR APPLICATION NUMBER:	60/090696
/	PRIOR FILING DATE:	1998-06-25
/	PRIOR APPLICATION NUMBER:	60/090862
/	PRIOR FILING DATE:	1998-06-26
/	PRIOR APPLICATION NUMBER:	60/090863
/	PRIOR FILING DATE:	1998-06-26
/	PRIOR APPLICATION NUMBER:	60/091360
/	PRIOR FILING DATE:	1998-07-01
/	PRIOR APPLICATION NUMBER:	60/091478
/	PRIOR FILING DATE:	1998-07-02
/	PRIOR APPLICATION NUMBER:	60/091544
/	PRIOR FILING DATE:	1998-07-01
/	PRIOR APPLICATION NUMBER:	60/091519
/	PRIOR FILING DATE:	1998-07-02
/	PRIOR APPLICATION NUMBER:	60/091626
/	PRIOR FILING DATE:	1998-07-02
/	PRIOR APPLICATION NUMBER:	60/091633
/	PRIOR FILING DATE:	1998-07-02
/	PRIOR APPLICATION NUMBER:	60/091978
/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/091982
/	PRIOR FILING DATE:	1998-07-07
/	PRIOR APPLICATION NUMBER:	60/092182
/	PRIOR FILING DATE:	1998-07-09

Query Match                100.0%; Score 713; DB 9; Length 713;  
 Best Local Similarity    100.0%; Pred.No 5e-161;

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Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy	61	TTTTGGGAATTTAATTTTCAAACAGCAGNAGTGACATTTTTCGTGCACATTTATTATT	120
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Qy	121	GTTGGTAGTGAAGCTATTGGAGATCCAAATTCAGGAAGCAACAACATTTGGAGAATGGCGTA	180
Dd	121	GTTGGTAGTGAAGCTATTGGAGATCCAAATTCAGGAAGCAACAACATTTGGAGAATGGCGTA	180
Qy	181	CTTTTCTATCAAGAAATAAAGAGAACCCAGTCAACCACCAACAATCATCTTTTAGAAGACAG	240
Dd	181	CTTTTCTATCAAGAAATAAAGAGAACCCAGTCAACCACCAACAATCATCTTTTAGAAGACAG	240
Qy	241	TGTGACTCTTACAAAAGCTGTCAAAACCAAGGCAAGGCCATAGTTAAAGGACGGAATCT	300
Dd	241	TGTGACTCTTACAAAAGCTGTCAAAACCAAGGCAAGGCCATAGTTAAAGGACGGAATCT	300
Qy	301	TGACTCAAGAGGGTTAAATCTTGTGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC	360
Dd	301	TGACTCAAGAGGGTTAAATCTTGTGTGTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACAC	360
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Dd	361	TTAGATTCAATGATTGTAAATTTAAGSCAAATACACATATTAGTATTACCTTAGTGTAAAT	420
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Dd	421	GTATCCCCTGTCAATATACAAATAGGTGAAMTTATTAAGTACCCCTATGCAGTTGGCTGCAC	480
Qy	481	AGTTCTAAATGGCACTTTATTAAATTTTAAATCAGTAACTGATTATTATCCTGGCTATGT	540
Dd	481	AGTTCTAAATGGCACTTTATTAAATTTTAAATCAGTAACTGATTATTATCCTGGCTATGT	540
Qy	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAAGTGTCTCTCCCC	600
Dd	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAAGTGTCTCTCCCC	600
Qy	601	TTACAGAAATGCACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGACATTAGAAAGG	660
Dd	601	TTACAGAAATGCACATTTTAAATGCGATACAGTTAGAAATAGGAAATATGACATTAGAAAGG	660



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 05:03:55 ; Search time 105 Seconds  
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3768.381 Million cell updates/sec

Title: US-09-989-293A-376  
Perfect score: 713  
Sequence: 1 aataatcatctattatca.....tattgccaaggaaaaaaa 713

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	75.2	10.5	528	3	US-08-772-440-7
3	46.6	6.5	7218	1	US-08-232-463-14
4	45.2	6.3	832	4	US-09-621-976-2813
5	44	6.2	640681	4	US-09-790-988-1
6	40.4	5.7	5847	4	US-09-920-672-10
7	39.6	5.6	20674	4	US-09-641-638-651
8	39.2	5.5	8920	2	US-08-446-855A-1
9	39.2	5.5	8920	3	US-08-150-741-1
10	38.6	5.4	4526	2	US-07-855-412B-4
11	38.6	5.4	4526	2	US-08-308-887A-4
12	38.6	5.4	4526	3	US-08-881-094-4
13	38.4	5.4	58407	4	US-08-916-421B-2
14	38	5.3	19233	4	US-10-204-708-45
15	37.8	5.3	1537	4	US-09-626-959D-2
16	37.8	5.3	202001	4	US-09-734-674-3
17	37.6	5.3	1335	4	US-09-543-681A-1450
18	37.4	5.2	275	4	US-08-585-593A-42
19	37.4	5.2	361	3	US-09-018-584A-9
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21	37.4	5.2	5852	1	US-07-867-106-2
22	37.4	5.2	786431	4	US-09-751-389-3
23	37.2	5.2	832	4	US-09-621-976-2813
24	37.2	5.2	9064	4	US-08-961-527-17
25	37	5.2	2110	3	US-09-419-459-1
26	37	5.2	10160	4	US-09-097-319A-8
27	37	5.2	10323	4	US-09-280-428A-11

C 28	37	5.2	11784	4	US-09-097-319A-9	Sequence 9, Appli
C 29	37	5.2	11991	4	US-09-097-319A-10	Sequence 10, Appl
C 30	37	5.2	24595	6	5428147-1	Patent No. 5428147
C 31	36.8	5.2	10467	4	US-10-204-708-2	Sequence 2, Appli
C 32	36.8	5.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
C 33	36.6	5.1	10640	4	US-09-417-485D-5	Sequence 5, Appli
C 34	36.6	5.1	11131	4	US-10-204-708-27	Sequence 27, Appl
C 35	36.6	5.1	51952	3	US-08-947-823-1	Sequence 1, Appli
C 36	36.4	5.1	408	4	US-09-134-001C-1464	Sequence 1464, Ap
C 37	36.4	5.1	1946	4	US-09-886-319A-83	Sequence 83, Appl
C 38	36.4	5.1	3331	3	US-09-042-785A-1	Sequence 1, Appli
C 39	36.4	5.1	161652	4	US-09-497-855A-40	Sequence 40, Appl
C 40	36.2	5.1	6113	4	US-10-204-708-14	Sequence 14, Appl
C 41	36	5.0	6317	4	US-10-204-708-11	Sequence 11, Appl
C 42	36	5.0	11050	4	US-10-204-708-86	Sequence 86, Appl
C 43	36	5.0	50000	4	US-09-146-053-3	Sequence 3, Appli
C 44	35.8	5.0	1634	4	US-09-220-132-111	Sequence 111, App
C 45	35.8	5.0	2570	2	US-09-056-075-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-772-440-1  
; Sequence 1, Application US/08772440  
; Patent No. 6046158  
; GENERAL INFORMATION:  
; APPLICANT: Ariizumi, Kiyoshi  
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772,440  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTXD:493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2298 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1966  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Y = C or T"  
US-08-772-440-1

Query March 10.9%; Score 77.6; DB 3; Length 2298;  
Best Local Similarity 73.1%; Pred. No. 8.5e-11;  
Matches 114; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 118 ATTGTTGGTATGTGAAGCTATTGGAGATCCATTGAGAACGACACATTCGAGAAATGG 177  
Db 274 AGTGCTGGGTGGCCTAGCAATTTGGCGCACAAATTCAGGAGAAATCCAGAGGAGAAAGA 333  
QY 178 CTACTTTCTATCAAGAAATAGAGAGAACACACAGTCAACCCACACAAATCATCTTTAGAAGA 237  
Db 334 CAATCTCTATCAAGAAATAGAGAGAACACACA---AGCCACAGAAATCATCTTTAGATGA 390  
QY 238 CAGTGTGACTCTTACCAAGCTGTCAAAACCCAGG 273  
Db 391 GAAGGTGGCTCCTCCCAAGGCACTCCCAAACTACAGG 426

## RESULT 2

US-08-772-440-7  
; Sequence 7, Application US/09772440  
; Patent No. 6046158  
; GENERAL INFORMATION:  
; APPLICANT: Ariizumi, Kiyoshi  
; APPLICANT: Takashima, Akira  
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
; TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/772,440  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTXD:493  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 528 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-772-440-7

Query Match 10.5%; Score 75.2; DB 3; Length 528;  
Best Local Similarity 77.2%; Pred. No. 2.3e-10;  
Matches 105; Conservative 0; Mismatches 28; Indels 3; Gaps 1;  
QY 138 TTGAGATCCAAATTCAGGAGAACACATTCGAGAAATGGCTACTTTCTATCAAGAAATA 197  
Db 2 TTTGGGACACAATTCAGGAGAAATCCAGAGGAGAAACAATTCCTATCAAGAAATA 61  
QY 198 AAGAGACCAAGTCAACCCACACATCTTTAGAGACAGTGTGACTCTCTACCAAG 257  
Db 62 AAGAGAACCA---AGCCACAGAAATCATCTTTAGATGAGAGGTGGCTCTCCCAAGG 118  
QY 258 CTGTCAAAACCAAGG 273  
Db 119 CATCCAAACTACAGG 134

## RESULT 3

US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: pTZ9pt-Fls  
US-08-232-463-14

Query Match 6.5%; Score 46.6; DB 1; Length 7218;  
Best Local Similarity 9.9%; Pred. No. 0.011;  
Matches 16; Conservative 98; Mismatches 47; Indels 0; Gaps 0;  
QY 553 AGGAGATCATATAATTGATACAAATAAGAAAGTGTTCTCTCCCTTACAGAAATGA 612  
Db 1456 AAGAGATAGAGAAATTTGCTACACACACACACACACACACACACACACACACACAC 1397  
QY 613 CATTTAAATGCGATACAGTTAGAAATAGGAAATATGACATTAAGAAAGAAATGACAGG 672  
Db 1396 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1337  
QY 673 GAGAAAGGAAAGGAGGAAATGTTCCCAAGGAAAAAAA 713  
Db 1336 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1296

## RESULT 4

US-09-621-976-2813  
; Sequence 2813, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

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Best Local Similarity 17.4%; Pred. No. 0.014;
Matches 40; Conservative 108; Mismatches 81; Indels 1; Gaps 1;

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QY 424 TCCTGTCTATATACATAAGTGAATTTAAGTACCTATGACCTATGCGCTGGACAGT 483
Db 209 KRCVSCSWGMSWKYMWWRWGNATGAGKAWRASCMWRKYAGKSKTSYKSMWMCW 268

QY 484 T-CTAATTCGACTTTATTAATTTTAAATCAGTAACTGATTATCACTGGCTATGTGC 542
Db 269 TRSKYCYTKARWTGYCYRKGGMWGRGWYASKYKMYMKRWCMWARMYRYSTGTRASM 328

QY 543 TTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAGTGT 592
Db 329 WWRWYTYMMKWKYAWARAAARWAWWAWRRACAAATATATATT 378

RESULT 5
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match      6.2%; Score 44; DB 4; Length 640681;
Best Local Similarity 54.3%; Pred. No. 0.19;
Matches 89; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

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QY 475 CTGACAGCTTCTAAATGGACTTTATTAAATTTTAAATCAGTAACTGATTTATCACTGG 534
Db 117569 GTTAAATATGATATATATGCTTTTAAATGAGTATATTTCTAAAGAGTTTATCTGT 117628

QY 535 CTATGTGCTTAGATCTCTACAGGAGATCATATAATTTTGATACAAAT 578
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Db 117629 TCATGGGATTAGTCTCCTACCTGTGTCATGATGATATTATTAATAATGAAT 117672

RESULT 6
US-09-920-672-10
; Sequence 10, Application US/09920672
; Patent No. 6455308
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/920,672
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 5847
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-920-672-10

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Best Local Similarity 68.3%; Pred. No. 0.41;
Matches 56; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 692 AATGTTGCCAAGGAAAAA 713
Db 1144 GCGAAGAAAGAAAGAGGAAA 1165

RESULT 7
US-09-641-638-651
; Sequence 651, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 651
; LENGTH: 20674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1123..3123
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 3124..3297
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 3871..4072
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OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5758..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5996..6099
OTHER INFORMATION: exon 5
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LOCATION: 6349..6509
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
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LOCATION: 12254..12340
OTHER INFORMATION: exon 9
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LOCATION: 12854..13023
OTHER INFORMATION: exon 10
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LOCATION: 13308..13429
OTHER INFORMATION: exon 11
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LOCATION: 16567..16667
OTHER INFORMATION: exon 12
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LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
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OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
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LOCATION: 8926  
OTHER INFORMATION: 10-349-368 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 12171  
OTHER INFORMATION: 10-350-72 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 12429  
OTHER INFORMATION: 10-350-332 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 13341  
OTHER INFORMATION: 10-507-170 : polymorphic base A or G  
NAME/KEY: allele  
LOCATION: 13492  
OTHER INFORMATION: 10-507-321 : polymorphic base A or C  
NAME/KEY: allele  
LOCATION: 13524  
OTHER INFORMATION: 10-507-353 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 13535

Query Match 5.6%; Score 39.6; DB 4; Length 20674;  
Best Local Similarity 56.0%; Pred. No. 0.96;  
Matches 75; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 464 TATGAGTTGGCTGGACAGTTCTTAAATTTGGACTTTTATTAATTTTAAATCAGTAACCTGA 523  
Db 10371 TTTCAGATGTCCTCACATGTTCCATGCTGAGGTTTAAAGGTTAAATGACTTAATGG 10430  
QY 524 TTATCACTGGCTATGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAG 583  
Db 10431 TGTGACACAGCTAAATGCTACAAAAACATTAGTCTTGCAAAATTTTTTTTTTCAGAG 10490  
QY 584 AAAAGTGTCTCTC 597  
Db 10491 ACAAGTCTCACTC 10504

RESULT 8  
US-08-446-855A-1  
Sequence 1, Application US/08446855A  
Patent No. 5849573  
GENERAL INFORMATION:  
APPLICANT: Stewart, Thomas S  
APPLICANT: Flores, Maria V  
APPLICANT: O'Sullivan, William J  
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl  
TITLE OF INVENTION: phosphate synthetase II  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Nixon & Vanderhye PC  
STREET: 1100 No. 5849573th Glebe Road, 8th Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
FILING DATE: 06-Jul-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mitchard, Leonard C  
REGISTRATION NUMBER: 29.009  
REFERENCE/DOCKET NUMBER: 47-80  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 8920 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic  
US-08-446-855A-1  
Query Match 5.5%; Score 39.2; DB 2; Length 8920;  
Best Local Similarity 46.6%; Pred. No. 0.95;  
Matches 162; Conservative 0; Mismatches 183; Indels 3; Gaps 1;  
QY 365 ATTCAATGATTGTAAATTTAAGGCAATAACACATATTAGTATTACCTTAGTGTAAATGAT 424  
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QY 425 CCCTGTCATATATACATAAGGTGAATTTATAGTACCTTATGAGTTCGCTGGACAGTT 484  
Db 478 AACCATCTATATATATACACAATATATAATCTCCCAATATTTGGTTCCTATAATT 537  
QY 485 CTAAATTTGGACTTTTATTAATTTTAAATCAGTAACCTGATTTATCACTGGCTATGCTT 544  
Db 538 TTATTTATATATTTTATTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTAT 594  
QY 545 AGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCTTAC 604  
Db 595 AAAATAGTAATCTACTAATTTTAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 654  
QY 605 AGAATTCACATTTTAAATGCGATACAGTTAGATAGGAATATGACATTAGAAGGAAGA 664  
Db 655 AAAATTTACATATGAAAAATGAACTTGTATATGTAATTTTATAAATTTTAAACATAAA 714  
QY 665 ATGACAGGGAAGGAAAGGAAAGGAAATGTTGCCAAGGAAAAA 712  
Db 715 TATAATGTATATAAAAAAAAAAAAAAAAAAGAAAAATATATATAGA 762

RESULT 9  
US-09-150-741-1  
Sequence 1, Application US/09150741  
Patent No. 6183996  
GENERAL INFORMATION:  
APPLICANT: Stewart et al.  
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate  
PATENT NO. 6183996  
TITLE OF INVENTION: Synthetase II  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/150,741  
CURRENT FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: PL6380  
EARLIER FILING DATE: 1992-12-16  
EARLIER APPLICATION NUMBER: AU93/00617  
EARLIER FILING DATE: 1993-12-02  
EARLIER APPLICATION NUMBER: 08/446,855  
EARLIER FILING DATE: 1995-07-06  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 8920  
TYPE: DNA  
ORGANISM: Plasmodium falciparum  
US-09-150-741-1

Query Match 5.5%; Score 39.2; DB 3; Length 8920;  
Best Local Similarity 46.6%; Pred. No. 0.95;  
Matches 162; Conservative 0; Mismatches 183; Indels 3; Gaps 1;  
QY 365 ATTCAATGATTGTAAATTTAAGGCAATAACACATATTAGTATTACCTTAGTGTAAATGAT 424  
Db 418 ATACAATTATTAAATTTTTCATGTTGACACATTAAATATAGTTTACACTTCTTATAATAA 477  
QY 425 CCCTGTCATATATACATAAGGTGAATTTATAGTACCTTATGAGTTCGCTGGACAGTT 484  
Db 478 AACCATCTATATATATACACAATATATAATCTCCCAATATTTGGTTCCTATAATT 537





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RESULT 12
US-08-881-094-4/c
; Sequence 4, Application US/08881094A
; Patent No. 6022739
; GENERAL INFORMATION:
; APPLICANT: Ryan, Clarence A
; APPLICANT: Pearce, Gregory L
; APPLICANT: McGurli, Barry F
; TITLE OF INVENTION: Systemin
; FILE REFERENCE: 7555-000001CPB
; CURRENT APPLICATION NUMBER: US/08/881,094A
; CURRENT FILING DATE: 1997-07-09
; EARLIER APPLICATION NUMBER: 08/308,887
; EARLIER FILING DATE: 1994-09-19
; EARLIER APPLICATION NUMBER: PCT/US93/02428
; EARLIER FILING DATE: 1993-03-18
; EARLIER APPLICATION NUMBER: 07/885,412
; EARLIER FILING DATE: 1992-03-19
; EARLIER APPLICATION NUMBER: 07/528,956
; EARLIER FILING DATE: 1990-05-25
; EARLIER APPLICATION NUMBER: PCT/US91/03685
; EARLIER FILING DATE: 1991-05-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 4526
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-08-881-094-4

Query Match          5.4%; Score 38.6; DB 3; Length 4526;
Best Local Similarity 48.4%; Pred. No. 1.1;
Matches 107; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 371 TGAATGTAATTTAAGCGAAATACACATATTAGTATTAATCCTTAGTGTAAATGATCCCTGT 430
Db 2108 TGAATGTAATTTAAGCGAAATACACATATTAGTATTAATCCTTAGTGTAAATGATCCCTGT 2049

QY 431 CATATATACAAATGAAGTGAAATTAAGTACCTGATCCCTAGTGGCTGGACAGTCTCAAT 490
Db 2048 GTAATATCTTTTAATTAATTAATTAATTTCCACAGTCTTAATTTATTATTAGTTTAAC 1989

QY 491 TGGACTTTATTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGCTTAGATCT 550
Db 1988 TGAACATAAAATTTTAAATAAATAGATGACTTAATGACGCAAAATTTGATATAAAGT 1929

QY 551 ACAGGAGATCATATATTTTCATACAAATAAAGAAAAGTGT 591
Db 1928 TTAAGTATGATCAATTAATTTTAAATAAATAGATGAATTAATGT 1888

RESULT 13
US-08-916-421B-2
; Sequence 2, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco-
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 58407
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (6485)..(6485)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-2

Query Match          5.4%; Score 38.4; DB 4; Length 58407;
Best Local Similarity 47.5%; Pred. No. 2.6;
Matches 114; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 346 TGTAAAGAAAACACCTTAGATTCATGATGTAATTTAAGGCAATACACATATTAGTA 405
Db 700 TATGAAAATATCCCTTTCAAAACAAATTAGATGTTATTAAAGGAAAGCTCAAAATCAATT 759

QY 406 TTACCTTAGTGAATGCTATCCCTGTCATATACATATAGGTGAATTAAGTACCCCTA 465
Db 760 AGATTTCTTTGAAGAATATTTCAATAAATTTGAAAAAATTTGGTATTTTCAATAAGAT 819

QY 466 TGCAGTTGGCTGGACAGTTCTAAATTTGGACTTTATTAAATTTTAAATCAGTAACTGATT 525
Db 820 GGAAAATAGTCGTTATTAATGAGCATATTAATCACTTCATCTCAATTAATATCATTT 879

QY 526 TATCACTGGCTATGCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAA 585
Db 880 GAGAGTAGATAAAGTGTGATATACGTTTAGAAGCTCAATAGACTACTACAATATAATAA 939

RESULT 14
US-10-204-708-45
; Sequence 45, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 45
; LENGTH: 19233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228).
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: unsure
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2004, 04:03:10 ; Search time 462 Seconds  
(without alignments)  
6556.202 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713

Sequence: 1 aatatatcatctattatca.....tggtgccaaggagaaaaaaa 713

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: geneseqn2000s:\*  
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7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	713	100.0	713	3	Aaz65094 Membrane-
2	713	100.0	713	3	Aac58634 Human PRO
3	713	100.0	713	4	Aas21480 Human CDN
4	713	100.0	713	5	Aaf44240 Human PRO
5	713	100.0	713	7	Abx77952 Human PRO
6	713	100.0	713	7	Abx80364 Novel hum
7	713	100.0	713	7	Abx9270 Human CDN
8	713	100.0	713	7	Abx24089 Novel hum
9	713	100.0	713	7	Abx90341 Human sec
10	713	100.0	713	7	Abx64187 cDNA enco
11	713	100.0	713	7	Abx67230 cDNA enco
12	713	100.0	713	7	Abx64409 Novel hum
13	713	100.0	713	7	Abx93839 cDNA enco
14	713	100.0	713	7	Abx89377 DNA enco
15	713	100.0	713	7	Abx80868 Human sec
16	713	100.0	713	7	Abx44377 cDNA enco
17	713	100.0	713	7	Abx42031 Human sec
18	713	100.0	713	7	Abx79548 Human sec
19	713	100.0	713	7	Abx93569 Novel hum
20	713	100.0	713	7	Abx81251 Novel hum
21	713	100.0	713	7	Abx94260 Human CDN
22	713	100.0	713	7	Abx93067 Novel hum
23	713	100.0	713	7	Abx17151 Human PRO

## ALIGNMENTS

## RESULT 1

Aaz65094  
ID AAZ65094 standard; cDNA; 713 BP.  
XX  
AC AAZ65094;  
XX  
DT 05-APR-2000 (first entry)  
XX  
DE Membrane-bound protein PRO1159 encoding cDNA.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO963088-A2.  
XX  
PD 09-DEC-1999.  
XX  
PF 02-JUN-1999; 99WO-US012252.  
XX  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
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PR 09-JUN-1998; 98US-0088722P.  
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Aca68006 Novel hum  
Aca88455 Human sec  
Acd81962 cDNA enco  
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Ada76423 Human PRO  
Ada19073 Human PRO  
Ada61696 Homo sapi  
Adb19481 Novel hum  
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PR 11-JUN-1998; 98US-00882909P.
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PR 24-JUN-1998; 98US-0090445P.
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PR 25-JUN-1998; 98US-0090676P.
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PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
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PR 04-AUG-1998; 98US-0095282P.
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PR 10-AUG-1998; 98US-0095329P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
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PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
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PR 19-AUG-1998; 98US-0097022P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
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PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

XX
XX
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX
XX WPI: 2000-072883/06.
XX P-PSDB; AAY66748.
XX
XX Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 271; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
XX
XX SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 713; DB 3; Length 713;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-155;
XX Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AATATATCATCTATTTATCATTAATCAATATGATTTATTTTATTCATTAACATTGGG 60
```

Db 1 AATATATCACTTATTTATCATTAATCAATAATGTAATCTTTATTCATTAACAATTTGGG 60  
QY 61 TTTTGGGATTTAATTTTCAAAACACAGCAGAAATGACATTTTCTGTGCTACTATTAATTT 120  
Db 61 TTTTGGGATTTAATTTTCAAAACACAGCAGAAATGACATTTTCTGTGCTACTATTAATTT 120  
QY 121 GTTGGTATGTAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180  
Db 121 GTTGGTATGTAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGAAATGGCTA 180  
QY 181 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCAACCCACCAATCATCTTTTGAAGACAG 240  
Db 181 CTTTCTATCAAGAAATAAAGAGAACCCACAGTCAACCCACCAATCATCTTTTGAAGACAG 240  
QY 241 TGTGCTCTCTACCAAGCTGTCAAAACACAGCAGGAGGATAGTTAAAGACGGAATCT 300  
Db 241 TGTGCTCTCTACCAAGCTGTCAAAACACAGCAGGAGGATAGTTAAAGACGGAATCT 300  
QY 301 TGAATCAAGAGGTTAATCTTGTGCTGAAGCTGGGCGAGGGTGAAGAAAAACAC 360  
Db 301 TGAATCAAGAGGTTAATCTTGTGCTGAAGCTGGGCGAGGGTGAAGAAAAACAC 360  
QY 361 TTAGATCAATGATTTAATTTAAGGCAATATACATATTTAGTATTTACCTTAGTGTAAAT 420  
Db 361 TTAGATCAATGATTTAATTTAAGGCAATATACATATTTAGTATTTACCTTAGTGTAAAT 420  
QY 421 GTATCCCTGTCAATATACATTAAGTGAATTTAATAGTACCCCTATGCTGCTGGAC 480  
Db 421 GTATCCCTGTCAATATACATTAAGTGAATTTAATAGTACCCCTATGCTGCTGGAC 480  
QY 481 AGTTCTAAATGGACTTTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGT 540  
Db 481 AGTTCTAAATGGACTTTAATTTTAAATCAGTAACTGATTTATCACTGGCTATGT 540  
QY 541 GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAAAAAGTGTCTCTCCC 600  
Db 541 GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAAAAAGTGTCTCTCCC 600  
QY 601 TTACAGAAATGACATTTTAAATGGATACAGTGTAGATAGGAATATGACATTAGAAAG 660  
Db 601 TTACAGAAATGACATTTTAAATGGATACAGTGTAGATAGGAATATGACATTAGAAAG 660  
QY 661 AAGAAATGACAGGAGAAAGAAAGGAAAAATGTTGCCAAGAAAAA 713  
Db 661 AAGAAATGACAGGAGAAAGGAAAGGAAAAATGTTGCCAAGAAAAA 713

## RESULT 2

AAC58634

ID AAC58634 standard; cDNA; 713 BP.

XX AC AAC58634;

XX AC AAC58634;

XX 29-JAN-2001 (first entry)

XX 29-JAN-2001 (first entry)

XX Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.

XX Human; immune related disease; diagnosis; anti-inflammatory; cardiant;  
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;  
KW antianemic; hepatotropic; virucide; antipsoriatic; antiallergic;  
KW antiaesthetic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopaenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.

OS Homo sapiens.

XX XX

PN WC200053758-A2.

XX XX

PD 14-SEP-2000.

XX XX

PF 02-MAR-2000; 2000WO-US005841.

XX XX

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99US-0123618P.

PR 12-MAR-1999; 99US-0123957P.

PR 23-MAR-1999; 99US-0125775P.

PR 12-APR-1999; 99US-0128849P.

PR 20-APR-1999; 99WO-US008615.

PR 28-APR-1999; 99US-0131445P.

PR 04-MAY-1999; 99US-0132371P.

PR 14-MAY-1999; 99US-0134287P.

PR 02-JUN-1999; 99WO-US012252.

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 03-OCT-1999; 99WO-US023089.

PR 29-OCT-1999; 99US-0162506P.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030999.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 11-FEB-2000; 2000WO-US000376.

PR 18-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004342.

XX XX

(GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

XX P-PSDB; AAB33469.

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Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 23; Fig 111; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and



CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy.  
XX  
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 4; Length 713;  
Best Local Similarity 100.0%; Pred. No. 2.7e-155;  
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AATATATCATCTATTATTCATTATTAATCAATATGATTTCTTTTATTCCTCAATTAACATTGGG 60  
Db 1 AATATATCATCTATTATTCATTATTAATCAATATGATTTCTTTTATTCCTCAATTAACATTGGG 60  
QY 61 TTTTGGGATTTTAAATTTTCAACACAGCAGCAATGACATTTTCTGTCACTATTATTATT 120  
Db 61 TTTTGGGATTTTAAATTTTCAACACAGCAGCAATGACATTTTCTGTCACTATTATTATT 120  
QY 121 GTTGATGATGAGCTATTGAGATCCAAATTCAGGAGCAACATTCCTGGGAGGATGGCTA 180  
Db 121 GTTGATGATGAGCTATTGAGATCCAAATTCAGGAGCAACATTCCTGGGAGGATGGCTA 180  
QY 181 CTTTCTATCAAGAAATAAGAGAACCCACAGTCAACCCACCAATCATCTTTAGAGACAG 240  
Db 181 CTTTCTATCAAGAAATAAGAGAACCCACAGTCAACCCACCAATCATCTTTAGAGACAG 240  
QY 241 TGTGACTCTACCAAGCTGTCAAAACACAGGAGGAGGCTAGTTAAGAGCGGAATCT 300  
Db 241 TGTGACTCTACCAAGCTGTCAAAACACAGGAGGAGGCTAGTTAAGAGCGGAATCT 300  
QY 301 TGACTCAAGAGGTTAAATTTCTTGGTGTGAGCCCTGGGCGAGGGGTAAAGAAAACAC 360  
Db 301 TGACTCAAGAGGTTAAATTTCTTGGTGTGAGCCCTGGGCGAGGGGTAAAGAAAACAC 360  
QY 361 TTGATTCATGATTTAAATTTAAGGCAAAATACATATTAGTATTACCTTAGTGTAAT 420  
Db 361 TTGATTCATGATTTAAATTTAAGGCAAAATACATATTAGTATTACCTTAGTGTAAT 420  
QY 421 GATCCCTGTCATATATCAATTAAGTGGAATTAAGTACCTATGAGTTGGCTGGAC 480  
Db 421 GATCCCTGTCATATATCAATTAAGTGGAATTAAGTACCTATGAGTTGGCTGGAC 480  
QY 481 AGTTCTAAATTCGACTTTTAAATTTTAAATTCAGTAACTGATTTATCCTGGCTATGT 540  
Db 481 AGTTCTAAATTCGACTTTTAAATTTTAAATTCAGTAACTGATTTATCCTGGCTATGT 540  
QY 541 GCTTAGATCTACAGGAGATCATATTTTGTATACAAATAAAGAAAGTGTCTCTCCCC 600  
Db 541 GCTTAGATCTACAGGAGATCATATTTTGTATACAAATAAAGAAAGTGTCTCTCCCC 600  
QY 601 TTACAGATTCGACTTTTAAATTCGATACAGTTAGTAAAGAAATATGACATTAGAAGG 660  
Db 601 TTACAGATTCGACTTTTAAATTCGATACAGTTAGTAAAGAAATATGACATTAGAAGG 660  
QY 661 AAGAATGACAGGAGAAAGGAGGAGGAAATGTTGCCAAGGAAAAAAA 713  
Db 661 AAGAATGACAGGAGAAAGGAGGAGGAAATGTTGCCAAGGAAAAAAA 713

RESULT 4

AAAF44240  
ID AAF44240 standard; cDNA; 713 BP.  
XX  
AC AAF44240;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
KW cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000WO-US008439.  
XX  
PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
(GETH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;  
PI Zhang Z;  
XX  
WPI; 2001-032160/04.  
P-PSDB; AAB65271.  
XX  
PT PRO polynucleotides used to produce polypeptides used to target bioactive  
PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
PT to cause targeted cell death.  
XX  
PS Claim 2; Fig 271; 935pp; English.  
XX  
CC The present invention describes human secreted and transmembrane PRO  
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
CC be used for targeted delivery of bioactive molecules, such as toxins,  
CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
CC sequences, and their fragments, can be used as hybridisation probes, in  
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
CC DNA. They may also be used to produce transgenic animals which are used  
CC to develop and screen therapeutically useful reagents. The PRO nucleotide

CC and protein sequence can be used for tissue typing and in treating  
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
 CC AAF44470 represent PCR primers and hybridisation probes used in the  
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to  
 CC AAF65300 represent human PRO polynucleotide and protein sequences given  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match	100.0%;	Score 713;	DB 5;	Length 713;
Best Local Similarity	100.0%;	Pred. No. 2.7e-155;		
Matches 713;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	AATATATCATCTATTTATCATTAATCAATTAATGATCTCTTTTATCCCAATAACATTTGGG	60
DB	1	AATATATCATCTATTTATCATTAATCAATTAATGATCTCTTTTATCCCAATAACATTTGGG	60
QY	61	TTTTGGGATTTAAATTTCAACACAGCAGAAATGACATTTTCTGTCATATTATTAT	120
DB	61	TTTTGGGATTTAAATTTCAACACAGCAGAAATGACATTTTCTGTCATATTATTAT	120
QY	121	GTGTGATGTCGAGCTATTTGAGATCCCAATTCAGGAACACACATTCGGAATGGCTA	180
DB	121	GTGTGATGTCGAGCTATTTGAGATCCCAATTCAGGAACACACATTCGGAATGGCTA	180
QY	181	CTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAGACAG	240
DB	181	CTTCTATCAAGAAATTAAGAGAACCCACAGTCAACCCACACATCATCTTTAGAGACAG	240
QY	241	TGTGACTCTACAAAGCTGTCAAAACACAGCAGGCGGCTAGTTAAAGACGGAATCT	300
DB	241	TGTGACTCTACAAAGCTGTCAAAACACAGCAGGCGGCTAGTTAAAGACGGAATCT	300
QY	301	TGACTCAAGAGGTTAAATCTTGGTCTGAAGCTGGGCGAGGGTAAAGAAAAACAC	360
DB	301	TGACTCAAGAGGTTAAATCTTGGTCTGAAGCTGGGCGAGGGTAAAGAAAAACAC	360
QY	361	TTAGATTCAATGATTTAAATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAT	420
DB	361	TTAGATTCAATGATTTAAATTAAGGCAAAATACACATATTAGTATTACCTTAGTGTAAT	420
QY	421	GTATCCCTCTCATATATCAATAAGGTGAATTAAGTACCCATGCGATGGCTGGAC	480
DB	421	GTATCCCTCTCATATATCAATAAGGTGAATTAAGTACCCATGCGATGGCTGGAC	480
QY	481	AGTTCTAAATGACATTTATTAATTTTAAATCAGTAATGATTTATCACTGGCTATCT	540
DB	481	AGTTCTAAATGACATTTATTAATTTTAAATCAGTAATGATTTATCACTGGCTATCT	540
QY	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTCTCTCCCC	600
DB	541	GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTCTCTCCCC	600
QY	601	TTACAGAATTGACATTTTAAATCGGATACAGTTAGGAATAGGAATGACATTAGAAAGG	660
DB	601	TTACAGAATTGACATTTTAAATCGGATACAGTTAGGAATAGGAATGACATTAGAAAGG	660
QY	661	AGAATGACAGGAGAAAGAAAGAGGAAATGTTGCCAGGAAAAA	713
DB	661	AGAATGACAGGAGAAAGAAAGAGGAAATGTTGCCAGGAAAAA	713

RESULT 5  
 ID ABX77952  
 AC ABX77952 standard; cDNA; 713 BP.  
 XX  
 AC ABX77952;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Human PRO polynucleotide #118.  
 XX  
 XX Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;

KW	liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW	antibody-dependent enzyme mediated prodrug therapy.
XX	Homo sapiens.
OS	US2003027163-A1.
PN	06-FEB-2003.
XX	15-NOV-2001; 2001US-00997666.
XX	16-JUN-1997; 97US-0049787P.
PR	17-OCT-1997; 97US-0062250P.
PR	05-NOV-1997; 97WO-US020069.
PR	12-NOV-1997; 97US-0065186P.
PR	13-NOV-1997; 97US-0065311P.
PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
PR	20-MAR-1998; 98US-0078910P.
PR	28-APR-1998; 98US-0083322P.
PR	07-MAY-1998; 98US-0084600P.
PR	28-MAY-1998; 98US-0087106P.
PR	02-JUN-1998; 98US-0087607P.
PR	02-JUN-1998; 98US-0087609P.
PR	02-JUN-1998; 98US-0087759P.
PR	03-JUN-1998; 98US-0087827P.
PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088025P.
PR	04-JUN-1998; 98US-0088028P.
PR	04-JUN-1998; 98US-0088028P.
PR	04-JUN-1998; 98US-0088029P.
PR	04-JUN-1998; 98US-0088030P.
PR	04-JUN-1998; 98US-0088033P.
PR	04-JUN-1998; 98US-0088326P.
PR	05-JUN-1998; 98US-0088167P.
PR	05-JUN-1998; 98US-0088202P.
PR	05-JUN-1998; 98US-0088212P.
PR	05-JUN-1998; 98US-0088217P.
PR	09-JUN-1998; 98US-0088659P.
PR	10-JUN-1998; 98US-0088734P.
PR	10-JUN-1998; 98US-0088738P.
PR	10-JUN-1998; 98US-0088742P.
PR	10-JUN-1998; 98US-0088810P.
PR	10-JUN-1998; 98US-0088824P.
PR	10-JUN-1998; 98US-0088826P.
PR	11-JUN-1998; 98US-0088858P.
PR	11-JUN-1998; 98US-0088861P.
PR	11-JUN-1998; 98US-0088876P.
PR	12-JUN-1998; 98US-0089105P.
PR	16-JUN-1998; 98US-0089440P.
PR	16-JUN-1998; 98US-0089512P.
PR	16-JUN-1998; 98US-0089514P.
PR	17-JUN-1998; 98US-0089532P.
PR	17-JUN-1998; 98US-0089538P.
PR	17-JUN-1998; 98US-0089598P.
PR	17-JUN-1998; 98US-0089599P.
PR	17-JUN-1998; 98US-0089653P.
PR	18-JUN-1998; 98US-0089801P.
PR	18-JUN-1998; 98US-0089907P.
PR	18-JUN-1998; 98US-0089908P.
PR	19-JUN-1998; 98US-0089947P.
PR	19-JUN-1998; 98US-0089948P.
PR	19-JUN-1998; 98US-0089952P.
PR	22-JUN-1998; 98US-0090246P.
PR	22-JUN-1998; 98US-0090252P.
PR	22-JUN-1998; 98US-0090254P.
PR	23-JUN-1998; 98US-0090349P.
PR	23-JUN-1998; 98US-0090355P.
PR	24-JUN-1998; 98US-0090429P.
PR	24-JUN-1998; 98US-0090431P.
PR	24-JUN-1998; 98US-0090435P.
PR	24-JUN-1998; 98US-0090444P.





```
QY 361 TTAGATTCATGATGTGTAATTTAAGGCAATATACATATTAGTATTACCTTAGTGTAA 420
Db |||||
QY 421 GTATCCCTGTCAATATACAAATAGGTGAATTAAGTACCCATGCGCTGGAC 480
Db |||||
QY 481 AGTTCTAAATTGCACTTTATTAAATTTTAAATCAGTAACTGATTTATCACTGGCTATGT 540
Db |||||
QY 541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAGTGTCTCTCCCC 600
Db |||||
QY 601 TTACAGAAATGACATTTTAAATCGGATACAGTTAGTAATAGGAATATGACATTAGAAAG 660
Db |||||
QY 661 AGAATGACAGGAGAGAAAGGAAAGGAAATGTTGCCAAGGAAAAAAA 713
Db |||||

RESULT 6
ID ABX80364
AC ABX80364;
XX
XX
XX 28-APR-2003 (first entry)
XX
XX Novel human secreted or transmembrane protein PRL124 DNA.
XX
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumour; immune response;
XX adrenal cortical capillary endothelial growth; c-fos induction;
XX vascular endothelial growth factor inhibition; VEGF inhibition;
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX retinal neurons cell survival; rod photoreceptor cell survival;
XX retinal disorder; retinitis pigmentosa; kidney disorder;
XX mammalian kidney mesangial cell proliferation; Berger disease;
XX dermatitis; herpiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
XX
XX Homo sapiens.
XX
XX
XX US2002132252-A1.
XX
XX 19-SEP-2002.
XX
XX 14-NOV-2001; 2001US-00990442.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
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XX 20-JUN-2001; 2001WO-US019692.
XX 29-JUN-2001; 2001WO-US021066.
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09-JUL-2001; 2001WO-US021735.  
28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P,  
Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NP,  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,  
Zhang Z;

WPI; 2003-247083/24.  
P-PSDB; ABU59165.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.

Claim 2; Fig 273; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1194 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO3536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1132, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of retinal neurons cells (PRO132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO813, PRO819 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide

Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred.No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels
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KW	cancerous tumour; immune response; retinal disorder; sight loss;			
KW	retinitis pigmentosa; age-related macular degeneration; AMD;			
KW	kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;			
KW	Crohn's disease; sports injury; arthritis.			
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PR 22-FEB-2000; 2000WO-US004414.
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RESULT 8

ACD24089

ID ACD24089 standard; cdna; 713 BP.

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XX AC ACD24089;
XX DT 26-AUG-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1159 cdna.
XX KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
XX KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
XX KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
XX KW TNF-alpha release; cell proliferation; cell differentiation;
XX KW gene expression modulator; proteoglycan release; cytokine release;
XX KW tumour; inflammatory disease; organ failure; atherosclerosis;
XX KW cardiac injury; infertility; birth defect; premature aging; AIDS;
XX KW acquired immunodeficiency syndrome; cancer; diabetic complication;
XX KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
XX KW bioreactor; tissue typing; gene; ss.
XX OS Homo sapiens.
XX PN US2003032156-A1.
XX PD 13-FEB-2003.
XX PF 06-MAY-2002; 2002US-00140474.
XX PR 31-MAR-1997; 97WO-US005230.
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XX PR 30-NOV-1999; 98WO-US028313.
XX PR 30-NOV-1999; 98WO-US028409.
XX PR 01-DEC-1999; 98WO-US028301.
XX PR 01-DEC-1999; 98WO-US028634.
XX PR 02-DEC-1999; 98WO-US028551.
XX PR 02-DEC-1999; 98WO-US028564.
XX PR 16-DEC-1999; 98WO-US030095.
XX PR 20-DEC-1999; 98WO-US030911.
XX PR 20-DEC-1999; 98WO-US030999.
XX PR 22-DEC-1999; 98WO-US030720.
XX PR 30-DEC-1999; 98WO-US031243.
XX PR 30-DEC-1999; 98WO-US031274.
XX PR 05-JAN-2000; 2000WO-US000219.
XX PR 06-JAN-2000; 2000WO-US000277.
XX PR 06-JAN-2000; 2000WO-US000376.
XX PR 11-FEB-2000; 2000WO-US003565.
XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.

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PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;  
XX  
XX WPI: 2003-341980/32.  
DR P-PSDB; ABO17852.  
DR  
XX  
XX New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, acquired immunodeficiency  
PT syndrome (AIDS), or cancer.  
XX  
XX Claim 2; Fig 473; 660pp; English.  
XX  
XX The invention describes an isolated nucleic acid (I) comprising, or which  
CC has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences

CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This sequence encodes a novel human secreted and transmembrane PRO  
CC polypeptide  
XX  
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;  
Query Match 100.0%; Score 713; DB 7; Length 713;  
Best Local Similarity 100.0%; Pred. No. 2.7e-155;  
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AATATATCATCTATTATCATTAATCAATATGATTTCTTTTATTCCTCAATACATTGGG 60  
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DB 61 TTTTGGGATTTAAATTTTCAACACAGCAGAAATGACATTTTCTGTCACTATTATT 120  
QY 121 GTTGGTATGTGAAGCTATTTCGAGATCCAAATTCAGGAAGCAACATTTGGAGATGGGTA 180  
DB 121 GTTGGTATGTGAAGCTATTTCGAGATCCAAATTCAGGAAGCAACATTTGGAGATGGGTA 180  
QY 181 CTTTCTATCAGAATAAAGAGAACCCACAGTCAACCCACAATCATCTTTAGAGACAG 240  
DB 181 CTTTCTATCAGAATAAAGAGAACCCACAGTCAACCCACAATCATCTTTAGAGACAG 240  
QY 241 TGTGACTCCTACAAAGCTGTCAAAACACAGGCAAGGCGATAGTTAAAGACGGAATCT 300  
DB 241 TGTGACTCCTACAAAGCTGTCAAAACACAGGCAAGGCGATAGTTAAAGACGGAATCT 300  
QY 301 TGACTCAGAGGGTTAAATTTCTGTGGCTGAGGCTGGGGCAGGGGTGTAAAGAAAACAC 360  
DB 301 TGACTCAGAGGGTTAAATTTCTGTGGCTGAGGCTGGGGCAGGGGTGTAAAGAAAACAC 360  
QY 361 TTAGATTCAATGATTTGTAATTTAAAGGCAATATACATATTAGTATTACCTTAGTGAAT 420  
DB 361 TTAGATTCAATGATTTGTAATTTAAAGGCAATATACATATTAGTATTACCTTAGTGAAT 420  
QY 421 GTATCCCTGTCAATATACATTAAGTGAATTTAAGTACCTTAGTGAATTTGGCTGGAC 480  
DB 421 GTATCCCTGTCAATATACATTAAGTGAATTTAAGTACCTTAGTGAATTTGGCTGGAC 480  
QY 481 AGTTCTTAAATTGGACCTTTTAAATTTTAAATCAGTAACCTGATTTATCAGTGGCTATGT 540  
DB 481 AGTTCTTAAATTGGACCTTTTAAATTTTAAATCAGTAACCTGATTTATCAGTGGCTATGT 540  
QY 541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAGTGTCTCTCCCC 600  
DB 541 GCTTAGATCTACAGGAGATCATATAATTTGATACAAATAAAGAAAAGTGTCTCTCCCC 600  
QY 601 TTACAGAAATTCACATTTTAAATGCGATACAGTGTAGAAATATGACATTAGAAAGG 660  
DB 601 TTACAGAAATTCACATTTTAAATGCGATACAGTGTAGAAATATGACATTAGAAAGG 660  
QY 661 AAGAATGACAGGAGAGAAAGGAGGAAAAGTGTCCCAAGGAAAAAAA 713  
DB 661 AAGAATGACAGGAGAGAGAAAGGAGGAAAAGTGTCCCAAGGAAAAAAA 713

CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This sequence encodes a novel human secreted and transmembrane PRO  
CC polypeptide

RESULT 9  
ABX90341  
ID ABX90341 standard; cDNA; 713 BP.  
XX  
AC ABX90341;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein cDNA, #154.  
XX  
KW Human; gene; ss; PRO; secreted; transmembrane; signal peptide;  
XX pharmaceutical; diagnostic; therapeutic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2002160384-A1.  
XX  
PD 31-OCT-2002.  
XX  
PF 14-NOV-2001; 2001US-00992598.  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
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PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
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PR 04-JUN-1998; 98US-0088029P.  
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PR 04-JUN-1998; 98US-0088033P.  
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PR 05-JUN-1998; 98US-0088167P.  
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PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
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PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
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PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Grissman MB, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napiet MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WL;  
PI Zhang Z;

WPI; 2003-288106/28.  
P-PSDB; ABU60595.

New transmembrane polypeptides and nucleic acids encoding the  
polypeptides, useful in gene therapy, in chromosome identification, as  
chromosome markers, or in generating probes.

Claim 2; Fig 271; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides  
comprising a sequence without signal peptide and the nucleic acid  
encoding them. The polypeptides can be used to raise antibodies that  
specifically bind to the PRO polypeptide, for linking a bioactive  
molecule to a cell expressing a PRO protein and for modulating at least  
one biological activity of a cell. The PRO polypeptides or  
polynucleotides are also useful in gene therapy, in chromosome  
identification, as chromosome markers, or in generating probes. The PRO  
polypeptides are useful as molecular markers for protein electrophoresis,  
and the isolated nucleic acids may be used for recombinantly expressing  
these markers. The PRO polypeptides and nucleic acids may also be used in  
tissue typing. Anti-PRO antibodies are useful in diagnostic assays for  
PRO, and in affinity purification of PRO from recombinant cell culture or

CC natural sources. The sequences presented in ABX90083-ABX90468 are the  
CC genes encoding, the primers amplifying and the probes detecting the PRO  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC is also available in electronic format from USPTO at  
CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

Query Match	100.0%;	Score 713;	DB 7;	Length 713;
Best Local Similarity	100.0%;	Pred. No. 2.7e-155;		
Matches 713;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AATATATCATCTATTTATTCATTAATCAATATGTAATCTCTTTATTCCAATAACAATTTGGG	60	
Db	1	AATATATCATCTATTTATTCATTAATCAATATGTAATCTCTTTATTCCAATAACAATTTGGG	60	
QY	61	TTTTGGGATTTTAATTTTCAAAACACAGCAGAAATGACATTTTCTTGTCGACTATTAATTTAT	120	
Db	61	TTTTGGGATTTTAATTTTCAAAACACAGCAGAAATGACATTTTCTTGTCGACTATTAATTTAT	120	
QY	121	GTTGGTATGTGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA	180	
Db	121	GTTGGTATGTGAAGCTATTTGGAGATCCAAATTCAGGAAGCAACACATTTGGAGATGGCTA	180	
QY	181	CTTTCTATCAAGAAATAAAGAGAACACACAGCTCAACCCACACAATATCTTTTGAAGACAG	240	
Db	181	CTTTCTATCAAGAAATAAAGAGAACACACAGCTCAACCCACACAATATCTTTTGAAGACAG	240	
QY	241	TGTGACTCTCTACCAAAAGCTCTGCAAAACCCACAGGCGAGGGCATAGTTTAAAGGACGGAACT	300	
Db	241	TGTGACTCTCTACCAAGCTCTCAAAACCCACAGGCGAGGGCATAGTTTAAAGGACGGAACT	300	
QY	301	TGACTCAAGAGGGTTAATCTCTGGTGCTGAAGCCTGGGCGAGGGGTGTAAGAGAAAACAC	360	
Db	301	TGACTCAAGAGGGTTAATCTCTGGTGCTGAAGCCTGGGCGAGGGGTGTAAGAGAAAACAC	360	
QY	361	TTAGATTCATGATTCGTAATTTTAAAGGCAATACACATATTAGTATTACCTTAGTGTAAAT	420	
Db	361	TTAGATTCATGATTTGTAATTTTAAAGGCAATACACATATTAGTATTACCTTAGTGTAAAT	420	
QY	421	GTATCCCTGTCATATATACAAATAGGTGAAATTTAAGTACCCTATTGACGTCGCTGGAC	480	
Db	421	GTATCCCTGTCATATATACAAATAGGTGAAATTTAAGTACCCTATTGACGTCGCTGGAC	480	
QY	481	AGTTCCTAAATGTGACCTTTATTAATTTTAAAAACAGTAACTGATTTATCACTGGCTATGT	540	
Db	481	AGTTCCTAAATGTGACCTTTATTAATTTTAAAAACAGTAACTGATTTATCACTGGCTATGT	540	
QY	541	GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAGAAAGTTCCTCTCCCC	600	
Db	541	GCTTAGATCTACAGGAGATCATATTAATTTGATACAAATAAAGAGAAAGTTCCTCTCCCC	600	
QY	601	TTACAGAAATTGACATTTTAAATGCGGATACAGTTAGAAATAGGAAATATGACATTTAGAAAGG	660	
Db	601	TTACAGAAATTGACATTTTAAATGCGGATACAGTTAGAAATAGGAAATATGACATTTAGAAAGG	660	
QY	661	AAAGATGACAGGAGAGAAAGAGAAAGAGGAAATGTTGCCAGGAAAAAATAA	713	
Db	661	AAAGATGACAGGAGAGAAAGAGAAAGAGGAAATGTTGCCAGGAAAAAATAA	713	

## RESULT 10

ABX64187

ID ABX64187 standard; cDNA: 713 BP.

XX

AC ABX64187;

XX

DT 26-FEB-2003 (first entry)

1000

DE CDNA























KW Human; PRO polypeptide; secreted protein; transmembrane protein; genetic disorder

genetic disorder; antibacterial; immunosuppressive; transgenic; transgenics

XX	gene therapy; gene; ss.
XX	
OS	Homo sapiens.
XX	
XX	US2002103125-A1.
XX	
XX	01-AUG-2002.
XX	
XX	20-NOV-2001; 2001US-00989731.
FF	
FF	16-JUN-1997; 97US-0049787B.
PR	17-OCT-1997; 97US-062250P.
PR	05-NOV-1997; 97WO-US0200069.
PR	12-NOV-1997; 97US-0065186P.
PR	13-NOV-1997; 97US-0065311P.
PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
PR	26-MAR-1998; 98US-0078910P.
PR	28-APR-1998; 98US-0083322P.
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PR	04-JUN-1998; 98US-0088028P.
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PR	12-JUN-1998; 98US-0089103P.
PR	16-JUN-1998; 98US-0089440P.
PR	16-JUN-1998; 98US-0089512P.
PR	16-JUN-1998; 98US-0089514P.
PR	17-JUN-1998; 98US-0089533P.
PR	17-JUN-1998; 98US-0089538P.
PR	17-JUN-1998; 98US-0089598P.
PR	17-JUN-1998; 98US-0089599P.
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PR	18-JUN-1998; 98US-0089907P.
PR	18-JUN-1998; 98US-0089968P.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	07-OCT-1998; 98WO-US021141.
PR	01-DEC-1998; 98WO-US025108.
PR	05-JAN-1999; 98WO-US000106.
PR	08-FEB-1999; 98WO-US000528.
PR	12-JUN-1999; 98WO-US012252.
PR	05-SEP-1999; 98WO-US021090.
PR	15-SEP-1999; 98WO-US021547.
PR	30-NOV-1999; 98WO-US028313.
PR	01-DEC-1999; 98WO-US028301.
PR	01-DEC-1999; 98WO-US028313.
PR	16-DEC-1999; 98WO-US030095.



PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX

(GETH ) GENENTECH LTD.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Giersten ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Kijavini ID, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart IA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-102117/09.  
 DR P-PSDB; ABU13977.  
 DR

XX Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 PT

PS Claim 2; Fig 271; 649pp; English.

CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for for  
 CC identifying agonists or antagonists. The polynucleotide sequences  
 CC encoding PRO polypeptides are useful as hybridisation probes, in  
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
 CC in the preparation of PRO polypeptides, for generating transgenic animals  
 CC or knockout animals, to construct hybridisation probes for mapping the  
 CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
 CC individuals with genetic disorders, in gene therapy, for chromosome  
 CC identification, as chromosome markers, and for generating probes for PCR,  
 CC Northern analysis, Southern analysis and Western analysis. The present  
 CC sequence encodes a human PRO polypeptide of the invention. Note: The  
 CC sequence data for this patent was obtained in electronic format directly  
 CC from the USPTO web site at seqdata.uspto.gov/psipdb/entry.html  
 XX

XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 7; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-155;

Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB |||||  
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 361 TTAGATTTCATGATTTAAATTTAGGCAAAATACACATATTAGTATTACCTTAGTCTAAT 420  
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 DB |||||  
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RESULT 11

ACA67230

ID ACA67230 standard; cDNA; 713 BP.

XX ACA67230;

AC ACA67230;

XX 23-JUN-2003 (first entry)

DT cDNA encoding human PRO polypeptide #237.

DE Human; PRO polypeptide; secreted and transmembrane protein;

XX anti-PRO antibody; diagnostic assay; gene expression; diabetes;

XX bone disorder; cartilage disorder; rheumatoid arthritis; obesity;

XX sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;

XX hearing loss; coagulation disorder; stroke; heart attack; cardiac;

XX antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;

XX antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.

XX Homo sapiens.

OS

XX US2003004311-Al.

PN 02-JAN-2003.

XX







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PR 08-MAR-1999; 99WO-US0005028.
PR 10-MAR-1999; 99WO-US0005190.
PR 20-APR-1999; 99WO-US0008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US011252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
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PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00860280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.

PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
XX P-P5DB; ABU66806.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
XX Claim 2; Fig 473; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
XX Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Query Match 100.0%; Score 713; DB 7; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.7e-155;
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATATCATCTATTATCAATTAATCAATATGTAATCTTTTATTCCTCAATACATTGGG 60
Db 1 AATATATCATCTATTATCAATTAATCAATATGTAATCTTTTATTCCTCAATACATTGGG 60
QY 61 TTTTGGGATTTTAAATTTCAACACAGCAGATGATGATTTTCTGTGCTACTATTATT 120
Db 61 TTTTGGGATTTTAAATTTCAACACAGCAGATGATGATTTTCTGTGCTACTATTATT 120
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Db 121 GTTGTATGTGAAGCTATTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTA 180
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Db 301 TGACTCAAGAGGGTTAAATCTTGCTGCTGAAGCTGGGGCAGGGGTGTTAAAGAAAAACAC 360
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Db 661 AAGAAATCAGAGGAGAGAAAGAGAGGAAATGTTGCCAAGAAAAAAA 713

RESULT 14
ABX89377
ID ABX89377 standard; cDNA; 713 BP.
XX AC ABX89377;
XX XX
XX DT 13-MAY-2003 (first entry)
XX DE
XX DE DNA encoding novel secreted and transmembrane protein PRO1159.
XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
XX cardiac insufficiency disorder; cancer; tumour; immune response;
XX adrenal cortical capillary endothelial growth; c-fos induction;
XX vascular endothelial growth factor inhibition; VEGF inhibition;
XX endothelial cell growth inhibitor; T-lymphocytes stimulation;
XX retinal neurons cell survival; rod photoreceptor cell survival;
XX retinal disorder; retinitis pigmentosa; kidney disease;
XX mammalian kidney mesangial cell proliferation; Berger disease;
XX dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX Homo sapiens.
XX OS
XX PN US2003017563-A1.
XX PD
XX PD 23-JAN-2003.
XX XX
XX PF 07-MAY-2002; 2002US-00140808.
XX XX
XX PR 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 14-SEP-1998; 98WO-US019094.
XX PR 16-SEP-1998; 98WO-US019177.
XX PR 16-SEP-1998; 98WO-US019330.
XX PR 17-SEP-1998; 98WO-US019437.
XX PR 07-OCT-1998; 98WO-US021441.
XX PR 29-OCT-1998; 98WO-US022991.
XX PR 20-NOV-1998; 98WO-US022992.
XX PR 01-DEC-1998; 98WO-US024855.
XX PR 05-JAN-1999; 98WO-US025108.
XX PR 08-MAR-1999; 99WO-US000106.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99WO-US005190.
XX PR 20-APR-1999; 99WO-US008615.
XX PR 14-MAY-1999; 99WO-US010733.
XX PR 02-JUN-1999; 99WO-US012252.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 08-SEP-1999; 99WO-US020594.
XX PR 13-SEP-1999; 99WO-US020944.
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XX PR 18-FEB-2000; 2000WO-US004341.
XX PR 18-FEB-2000; 2000WO-US004342.
XX PR 22-FEB-2000; 2000WO-US004414.
XX PR 24-FEB-2000; 2000WO-US004914.
XX PR 24-FEB-2000; 2000WO-US005004.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005746.
XX PR 02-MAR-2000; 2000WO-US005841.
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XX PR 15-MAR-2000; 2000WO-US006884.
XX PR 20-MAR-2000; 2000WO-US007377.
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XX PR 02-JUN-2000; 2000WO-US015264.
XX PR 28-JUL-2000; 2000WO-US020710.
XX PR 11-AUG-2000; 2000WO-US022031.
XX PR 23-AUG-2000; 2000WO-US023522.
XX PR 24-AUG-2000; 2000WO-US023328.
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XX PR 20-DEC-2000; 2000WO-US034956.
XX PR 28-FEB-2001; 2001US-00796498.
XX PR 28-FEB-2001; 2001WO-US006520.
XX PR 01-MAR-2001; 2001WO-US006566.
XX PR 09-MAR-2001; 2001US-00802706.
XX PR 14-MAR-2001; 2001US-00808589.
XX PR 22-MAR-2001; 2001US-00816744.
XX PR 03-APR-2001; 2001US-00828366.
XX PR 10-MAY-2001; 2001US-00854208.
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XX PR 18-MAY-2001; 2001US-00860216.
XX PR 25-MAY-2001; 2001US-00866028.
XX PR 25-MAY-2001; 2001US-00868034.
XX PR 25-MAY-2001; 2001WO-US017092.
XX PR 01-JUN-2001; 2001US-00872035.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 05-JUN-2001; 2001US-00874503.
XX PR 14-JUN-2001; 2001US-00882636.
XX PR 19-JUN-2001; 2001US-00886342.
XX PR 20-JUN-2001; 2001WO-US019692.
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PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
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PR 24-JUN-1998; 98US-0090472P.  
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PR 24-JUN-1998; 98US-0090542P.  
PR 24-JUN-1998; 98US-0090557P.  
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PR 25-JUN-1998; 98US-0090694P.  
PR 25-JUN-1998; 98US-0090695P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
PR 02-JUL-1998; 98US-0091519P.  
PR 02-JUL-1998; 98US-0091626P.  
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PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
PR 07-JUL-1998; 98US-0091982P.  
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PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 16-SEP-1998; 98WO-US019330.  
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PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 12-MAR-1999; 99US-0123957P.  
PR 02-JUN-1999; 99WO-US012252.  
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PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.



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PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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8	186	26.1	221471	2	AC006510 Homo sapi
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11	140	19.6	625	9	AF400602 Homo sapi
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AR252626  
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REFERENCE Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,  
AUTHORS Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,  
Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J.,  
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Williams, P., Wood, W.I. and Zhang, Z.  
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REFERENCE Baker, K.P., Beresini, M., Defoige, L., Desnovers, L., Filvaroff, E.,  
AUTHORS Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Wood, W.I. and Zhang, Z.  
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AUTHORS Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B.,
Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E.,
Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S.,
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Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,
Goddard W., Wood W.I. and Godowski P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
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A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
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Direct Submission
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RESULT 6
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LOCUS Homo sapiens 12 BAC RP11-133L14 (Roswell Park Cancer Institute
DEFINITION Human BAC Library) complete sequence.
ACCESSION AC024224
VERSION AC024224.33 GI:21240476
KEYWORDS HTG
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 165414)
AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C.,
Alsbrooks S.L., Amaratunga H.C., Are J.R., Ayele M., Banks T.,
Barbieri J., Benton J., Binage K., Blankenburg K., Bonnin D.,
Bouck J., Bowe S., Brieva M., Brown E., Brown M., Bryant N.P.,
Buahay C., Burch P., Burkett C., Burrell K.L., Byrd N.C.,
Carroll T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,
Chen G., Chen R., Chen Z., Chiu D., Chowdhry I., Christopoulos C.,
Cleveland C.D., Cox C., Coyle M.D., Dathorne S.R., David R.,
Davila M.L., Davis C., Davy-Carroll L., Dederich D.A.,
Delaney K.R., Delgado O., Denn A.L., Ding Y., Dinin H.H.,
Douthwaite K.J., Draper H., Dugan-Rocha S., Durbin K.J.,
Earhart C., Edgar D., Edwards C.C., Elhaj C., Emerling S.,
Escotto M., Falls T., Ferraguto D., Flagg N., Ford J., Foster P.,
Frantz P., Gabisi A., Gao J., Garcia A., Garner T., Garza N.,
Gill R., Gorrell J.H., Guevara W., Gunaratne P., Hale S.,
Hamilton K., Han J., Harris C., Harris K., Hart M., Havlak P.,
Hawes A., Hernandez J., Hernandez O., Hodgson A., Hogues M.,
Holloway C., Hollins B., Honsi F., Howard S., Huber J., Hulyk S.,
Hume J., Ioshikhes I., Jackson L.E., Jacobson B., Jia Y.,
Johnson R., Jolivet S., Joudah S., Karlsson E., Kelly S., Khan U.,
King L., Korvah J., Kovar C., Kratovic J., Kurehi A., Landry N.,
Leal B., Lee E., Lewis L., Lewis L., Li J., Li Z., Lichtarge O.,
Lieu C., Liu J., Liu W., Loulseged H., Lozado R.J., Lu X.,
```

Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Fu, J.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scher, S., Scott, G., Shen, H., Shim, C., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstein, G. and Gibbs, R.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 165414)  
Worley, K.C.  
Direct Submission  
Submitted (28-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 165414)  
Worley, K.C.  
Direct Submission  
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 165414)  
Worley, K.C.  
Direct Submission  
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base

quality are listed below. Description of the metrics can be found at URL:  
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES  
source

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Matches 708; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 61 TTTTGGGATTTAATTTTCAACACACAGCAGATGACATTTTCTGTCTACTATTATT 120
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## RESULT 7

AC006510/c

LOCUS

DEFINITION

AC006510 AC006514

AC006510.8 GI:10122018

HTG: HTGS PHASE1

Homo sapiens

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 240864)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,

Alabrooks, S.L., Amarantunge, H.C., Are, J.R., Banks, T., Barbaccia, J.,

Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowles, S., Brieve, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,

Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,

Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,

Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,

Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C.,

Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J.,

Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,

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Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Holloway, C.,

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Jackson, L.E., Jacobson, E., Jia, Y., Johnson, R., Jolivet, S.,

Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,

Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,

Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,

Loulsegh, H., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,

Ma, J., Maheshwari, N., Mapua, P., Martin, R., Martindale, A.,

Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M.,

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Morgan, A., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N.,

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Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,

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Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,

and Gibbs, R.

Direct Submission

Unpublished

2 (bases 1 to 240864)

Worley, K.C.

Direct Submission

Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 14, 2000 this sequence version replaced gi:10086352.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: J-33

Center clone name: RP11-13C13, RP11-656E20

----- Summary Statistics

Sequencing vector: Plasmid; M77789

Sequencing vector: M13; L08921

Chemistry: Dye-primer Bodipy: 77% of reads

Chemistry: Dye-terminator Big Dye: 23% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 71594 bases at least Q40  
Consensus quality: 93014 bases at least Q30  
Consensus quality: 110702 bases at least Q20  
Estimated insert size: 229041; sum-of-contigs estimation  
Estimated insert size: 331000; agarose-fp estimation  
Quality coverage: 0.6x in Q20 bases; agarose-fp estimation  
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 111085: contig of 111085 bp in length  
\* 111086 111185: gap of unknown length  
\* 111186 134782: contig of 23597 bp in length  
\* 134782 134883: gap of unknown length  
\* 134883 163654: contig of 28772 bp in length  
\* 163654 163754: gap of unknown length  
\* 163754 185050: contig of 21296 bp in length  
\* 185050 185151: gap of unknown length  
\* 185151 194802: contig of 9652 bp in length  
\* 194802 202527: contig of 7625 bp in length  
\* 202527 202628: gap of unknown length  
\* 202628 208658: contig of 6031 bp in length  
\* 208658 208758: gap of unknown length  
\* 208758 221786: contig of 13027 bp in length  
\* 221786 230142: contig of 8257 bp in length  
\* 230142 230242: gap of unknown length  
\* 230242 232625: contig of 2383 bp in length  
\* 232625 232725: gap of unknown length  
\* 232725 234559: contig of 1734 bp in length  
\* 234559 234560: gap of unknown length  
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\* 235821 235922: gap of unknown length  
\* 235922 237146: contig of 1225 bp in length  
\* 237146 237247: gap of unknown length  
\* 237247 238417: contig of 1171 bp in length  
\* 238417 238517: gap of unknown length  
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DEFINITION SEQUENCE, 13 unordered pieces.  
AC138620  
AC138620.2 GI:28557995  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 221471)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 221471)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Direct Submission  
REFERENCE 3 (bases 1 to 221471)  
AUTHORS McPherson,J.D. and Waterston,R.H.  
TITLE Direct Submission  
JOURNAL Direct Submission  
COMMENT Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
On Feb 25, 2003 this sequence version replaced gi:27657609.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu/gsc/index.shtml>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
----- Project Information -----



Center project name: M\_BA0250E01

Summary Statistics

Sequencing vector: M13; 0%  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 217739 bases at least Q40  
Consensus quality: 218068 bases at least Q30  
Consensus quality: 218373 bases at least Q20  
Insert size: 193000; agarose-fp  
Insert size: 227132; sum-of-contigs  
Quality coverage: 14.88 in Q20 bases; agarose-fp  
Quality coverage: 12.33 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1509: contig of 1509 bp in length  
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20221 20320: gap of unknown length  
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33396 33496: gap of unknown length  
33496 46731: contig of 13236 bp in length  
46732 46832: gap of unknown length  
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62519 80892: gap of unknown length  
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LOCUS Rattus norvegicus clone CH230-94G2, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
DEFINITION 2 unordered pieces.

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 HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 ORGANISM

1 (bases 1 to 273867)  
 Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,  
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 Weinstock,G. and Gibbs,R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 273867)  
 Worley,K.C.  
 Direct Submission  
 Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 273867)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Oct 10, 2002 this sequence version replaced gi:21737395.

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\*\*\*\*\* Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 Project Information  
 Center project name: GPBG  
 Center clone name: CH230-94G2  
 Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 244419 bases at least Q40  
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 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html)  
 \* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 271836: contig of 271836 bp in length  
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 \* 271937 273867: contig of 1931 bp in length.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 625)  
Willment, J.A., Gordon, S. and Brown, G.D.  
Characterization of the human beta -glucan receptor and its  
alternatively spliced isoforms  
J. Biol. Chem. 276 (47), 43818-43823 (2001)  
21570237  
PUBMED 11567029  
2 (bases 1 to 625)  
Willment, J.A., Gordon, S. and Brown, G.D.  
Direct Submission  
Submitted (18-JUL-2001) Sir William Dunn School of Pathology,  
Oxford University, South Parks Road, Oxford OX1 3RE, UK  
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Homo sapiens beta-glucan receptor isoform H (BGR) mRNA, complete  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 881)  
Willment, J.A., Gordon, S. and Brown, G.D.  
Characterization of the human beta -glucan receptor and its  
alternatively spliced isoforms  
J. Biol. Chem. 276 (47), 43818-43823 (2001)  
21570237  
PUBMED 11567029  
2 (bases 1 to 881)  
Willment, J.A., Gordon, S. and Brown, G.D.  
Direct Submission  
Submitted (18-JUL-2001) Sir William Dunn School of Pathology,  
Oxford University, South Parks Road, Oxford OX1 3RE, UK  
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REFERENCE	1 (bases 1 to 744)
AUTHORS	Willment,J.A.; Gordon,S. and Brown,G.D.
TITLE	Characterization of the human beta -glucan receptor and its alternatively spliced isoforms
JOURNAL	J. Biol. Chem. 276 (47), 43818-43823 (2001)
MEDLINE	21570237
PUBMED	11567029
REFERENCE	2 (bases 1 to 744)
AUTHORS	Willment,J.A., Gordon,S. and Brown,G.D.
TITLE	Direct Submission
JOURNAL	Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
MEDLINE	Oxford University, South Parks Road, Oxford OX1 3RE, UK
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VERSION	AY026769.2 GI:15967096
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1 (bases 1 to 744)	
Hermanz-Falcon,P., Arce,I., Roda-Navarro,P. and Fernandez-Ruiz,E.B.	
Cloning of human DEC1N-1, a novel C-type lectin-like receptor gene expressed on dendritic cells	
Immunogenetics 53 (4), 288-295 (2001)	
JOURNAL	Medline 21383615
PUBMED	11491532

REFERENCE 2 (bases 1 to 744)  
AUTHORS Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.  
TITLE Direct Submission  
JOURNAL Submitted (01-FEB-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain  
REFERENCE 3 (bases 1 to 744)  
AUTHORS Herranz-Falcon,P., Arce,I. and Fernandez-Ruiz,E.  
TITLE Direct Submission  
JOURNAL Submitted (05-OCT-2001) Biologia Molecular, Hospital de la Princesa, Diego de Leon 62, Madrid 28006, Spain  
REMARK Sequence update by submitter  
COMMENT On Oct 5, 2001 this sequence version replaced gi:14278818.  
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Job time : 3359 secs

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DEFINITION Homo sapiens beta-glucan receptor isoform G (BGR) mRNA, complete cds, alternatively spliced.  
ACCESSION AF400601  
VERSION AF400601.1 GI:15986711  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 787)  
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.  
TITLE Characterization of the human beta -glucan receptor and its alternatively spliced isoforms  
J. Biol. Chem. 276 (47), 43818-43823 (2001)  
JOURNAL 21570237  
MEDLINE 11567029  
PUBMED  
REFERENCE 2 (bases 1 to 787)  
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.  
TITLE Direct Submission

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 4, 2004, 09:09:43 ; Search time 385 Seconds

(without alignments)

874.330 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

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Total number of hits satisfying chosen parameters: 4932372

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

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; Sequence 376, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC63  
CURRENT APPLICATION NUMBER: US/09/989,722  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PLC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
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Score: 462.00 Matches: 90  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
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RESULT 2  
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Sequence 376, Application US/09989723  
Patent No. US20020072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.



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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:  
Pred. No.: 3,38e-57 Length: 713  
Score: 462.00 Matches: 90  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-723-376 (1-713)

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Db 152 TCAGGAAGCAACACATTGGAGATGGCTACTTCTATCAAGAAATAAGAGAACACACAGT 211  
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; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Napier, Mary A.

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; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C56

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; CURRENT FILING DATE: 2001-11-19

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60/089976	PRIOR FILING DATE: 1998-07-07

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; PRIOR FILING DATE: 1998-07-09
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; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
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Db 152 TCAGGAGACACACATTTGGAGATGGCTACTTCTATCAAGAAATAAAGAACACACAGT 211  
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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
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## RESULT 6

US-09-989-732-376  
; Sequence 376, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C57  
CURRENT APPLICATION NUMBER: US/09/989,732  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C15  
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CURRENT FILING DATE: 2001-11-14  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-732-376 (1-713)

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DB 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACA 271  
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DB 272 GCGAAGGGGATGTTAAAGAGCGGAATCTTGACTCAAGAGGGTTAATCTTGTGTCTGAA 331  
QY 81 AlaTyrGlyArgGlyValLysLysAsnThr 90  
DB 332 GCGTGGGGGCGGGGTGTAAAGAAAACACT 361

## RESULT 7

US-09-991-073-376

Sequence 376, Application US/09991073

Patent No. US20020127576A1

GENEAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter



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Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-991-073-376 (1-713)

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Db 332 GCCTGGGCGAGGGGTGTTAAGAAAAACACT 361
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RESULT 8  
US-09-990-442-376  
Sequence 376, Application US/09990442  
Patent No. US20020132252A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Fong, Sherman  
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APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C8  
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 3.28e-57
Score: 462.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 9
Gaps: 0

US-09-989-293A-377 (1-90) x US-09-990-442-376 (1-713)

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Db 152 TCAGGAGCAACACATTCGAGATTCGCTATCTTCTATCAAGAAATAAGAGAACACAGT 211
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Db 212 CAACCCACACATCATCTTTTGAAGACAGTGTGACTCTCCACAAAGCTGTCAAAACCACA 271
Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GGCAGGCGCATAGTTAAAGGACGGATCTTGACTCAAGAGGGTTAATCTTGTGCTGAA 331
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Db 332 GCGTGGGCGAGGGGTGTAAAGAAAACACT 361

RESULT 9
US-09-991-163-376
; Sequence 376, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-02

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Pred. No.: 3,38e-57 Length: 713
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Query Match: 100.00% Indels: 0
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DB 272 GCCAAGGGCATAGTTAAGACAGGATCTTGACTCAAGAGGGTAAATCTTGTGCTGAA 331
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DB 332 GCCTGGGGCAGGGGTGTAAAGAAAACACT 361

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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.:      3,38e-57      Length:      713
Score:          462.00      Matches:     90
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             9          Gaps:         0

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QY      21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnIleHisSer 40
Db      152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTTATCAAGAAATAAAGAGAACCCACAT 211
QY      41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValIlyThrThr 60
Db      212 CAACCCACACATCATCTTTAGAGACAGTGTGATCTCTACCAAGCTGTCAAAACCACA 271
QY      61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGlu 80
Db      272 GGCAAGGGCATAGTTAAAGACGGAATCTTGACTCAAGAGGGTTAATCTTGGTGTCTGAA 331
QY      81 AlaTrpGlyArgGlyValIlyLysAsnThr 90
Db      332 GCGTGGGGCAGGGGTGTAAAGAAAACACT 361

RESULT 11
US-09-990-456-376
; Sequence 376, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zeman
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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1 / TITLE OF INVENTION: Acids Encoding the Same  
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4 / CURRENT FILING DATE: 2001-11-14  
5 / PRIOR APPLICATION NUMBER: 60/049787  
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC55  
CURRENT APPLICATION NUMBER: US/09/989,721  
CURRENT FILING DATE: 2001-11-19  
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Db 212 CAACCCACACAATCATCTTTAGAGACAGTGTGACTCTTACCAAGCTGTCAAACCCACA 271  
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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
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## RESULT 12

US-09-989-721-376  
Sequence 376, Application US/09989721  
Patent No. US20020142961A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.



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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC20  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

## Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-992-598-376 (1-713)

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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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61	PRIOR APPLICATION NUMBER: 60/091633
62	PRIOR FILING DATE: 1998-07-02
63	PRIOR APPLICATION NUMBER: 60/091978
64	PRIOR FILING DATE: 1998-07-07
65	PRIOR APPLICATION NUMBER: 60/091982
66	PRIOR FILING DATE: 1998-07-07
67	PRIOR APPLICATION NUMBER: 60/092182
68	PRIOR FILING DATE: 1998-07-09

Alignment Scores:	
Pred. No.:	3.38e-57
Score:	462.00
Length:	713
Matches:	90
Conservative:	0
Percent Similarity:	100.00%

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-989-293A-377 (1-90) x US-09-989-293A-376 (1-713)

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QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40  
DB 152 TCAGGAAGCACACACATTGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCACT 211  
QY 41 GinProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
DB 212 CACCCACACAAATCATCTTTAGAGACAGTGTGACTCCACCAAGCTGTCAAAACCA 271  
QY 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGlu 80  
DB 272 GGCAGGGCATAGTTAAAGACGGAATCTTGACTCAGAGGGTTAATCTTGGTGTGAA 331  
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
DB 332 GCCTGGGGCAGGGTGTAAAGAAAAACACT 361

RESULT 15

US-09-989-735-376  
; Sequence 376, Application US/09989735  
; Publication No. US20020193299A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730P1C61  
; CURRENT APPLICATION NUMBER: US/09/989,735  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/065186  
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;; PRIOR FILING DATE: 1998-07-09

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Job time : 387 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: April 4, 2004, 07:58:52 ; Search time 89 Seconds  
(without alignments)

561.186 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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3	70.5	15.3	Sequence 7, Appli
4	69.5	15.0	Sequence 3, Appli
5	69.5	15.0	Sequence 243, App
6	67.5	14.6	Sequence 183, App
7	67	14.5	Sequence 1899, Ap
8	67	14.5	Sequence 35, Appl
9	67	14.5	Sequence 35, Appl
10	67	14.5	Sequence 34, Appl
11	67	14.5	Sequence 34, Appl
12	66.5	14.4	Sequence 16320, A

C 13	66.5	14.4	1332	4	US-09-252-991A-15961	Sequence 15961, A
C 14	65.5	14.2	548	4	US-09-621-976-3007	Sequence 3007, Ap
C 15	65.5	14.2	744	4	US-09-134-000C-2940	Sequence 2940, Ap
C 16	65.5	14.2	1341	4	US-09-252-991A-16544	Sequence 16544, A
C 17	65	14.1	1386	4	US-09-134-001C-767	Sequence 767, App
C 18	65	14.1	2003	4	US-09-148-545-109	Sequence 109, App
C 19	65	14.1	2070	4	US-09-148-545-51	Sequence 51, Appl
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C 21	65	14.1	5833	4	US-09-976-594-183	Sequence 183, App
C 22	65	14.1	41708	4	US-09-470-512A-3	Sequence 3, Appli
C 23	64.5	14.0	1068	4	US-09-328-352-434	Sequence 434, App
C 24	64.5	14.0	35060	3	US-08-814-095-7	Sequence 7, Appli
C 25	64	13.9	3501	1	US-08-448-170-5	Sequence 5, Appli
C 26	64	13.9	3501	3	US-08-961-803-4	Sequence 4, Appli
C 27	64	13.9	3507	4	US-09-661-322A-21	Sequence 21, Appli
C 28	64	13.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
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C 30	63.5	13.7	1215	4	US-09-594-506-29	Sequence 29, Appl
C 31	63.5	13.7	2646	4	US-09-489-039A-4832	Sequence 4832, Ap
C 32	63	13.6	729	3	US-08-998-416-994	Sequence 994, App
C 33	63	13.6	948	4	US-09-134-001C-1418	Sequence 1418, Ap
C 34	63	13.6	1499	3	US-09-300-672-3	Sequence 3, Appli
C 35	63	13.6	1500	3	US-09-300-672-1	Sequence 1, Appli
C 36	63	13.6	3214	1	US-08-484-105-17	Sequence 17, Appl
C 37	63	13.6	3214	1	US-08-484-106-17	Sequence 17, Appl
C 38	62.5	13.5	2409	4	US-09-484-970B-101	Sequence 101, App
C 39	62	13.4	2336	1	US-08-247-948A-1	Sequence 1, Appli
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C 45	61.5	13.3	875	2	US-08-778-912A-2	Sequence 2, Appli

# ALIGNMENTS

## RESULT 1

US-08-772-440-1  
; Sequence 1, Application US/08772440  
; Patent No. 6046158

; GENERAL INFORMATION:

; APPLICANT: Ariizumi, Kiyoshi

; APPLICANT: Takashima, Akira

; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE

; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/772,440

; FILING DATE: CONCURRENTLY HERewith

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Parker, David L.

; REGISTRATION NUMBER: 32,165

; REFERENCE/DOCKET NUMBER: UTXD:493

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 512/418-3000

; TELEFAX: 512/474-7577

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

LENGTH: 2298 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 1966  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Y = C or T"  
US-08-772-440-1

Alignment Scores:  
Pred. No.: 9,48e-10 Length: 2298  
Score: 143.50 Matches: 29  
Percent Similarity: 74.47% Conservatives: 6  
Best Local Similarity: 61.70% Mismatches: 11  
Query Match: 31.06% Indels: 1  
DB: Gaps: 1

US-09-989-293A-377 (1-90) x US-08-772-440-1 (1-2298)

QY 15 AlaileTTPArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34  
DB 290 GCATTTGGCGACACAAATTCAGGAGAAATCCAGAGGAGAAAGACAACTTCCTATCAAGA 349  
QY 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54  
DB 350 AATAAGAGAGAACACAC--AAGCCACAGAAATCATCTTTAGATGAGAGAGGTGGCTCCCTCC 406  
QY 55 LysAlaValLysThrThrGly 61  
DB 407 AAGGCATCCCAACTACAGGA 427

RESULT 2  
US-08-772-440-7  
Sequence 7, Application US/08772440  
Patent No. 6046158  
GENERAL INFORMATION:  
APPLICANT: Ariizumi, Kiyoshi  
APPLICANT: Takashima, Akira  
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772.440  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTXD:493  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 528 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-772-440-7

Alignment Scores:  
Pred. No.: 3,64e-10 Length: 528  
Score: 139.50 Matches: 28  
Percent Similarity: 75.56% Conservatives: 6  
Best Local Similarity: 62.22% Mismatches: 10  
Query Match: 30.19% Indels: 1  
DB: Gaps: 1

US-09-989-293A-377 (1-90) x US-08-772-440-7 (1-528)

QY 17 TTPArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLys 36  
DB 4 TGGCGACACAAATTCAGGAGAAATCCAGAGGAGAAAGACAACTTCCTATCAAGAAATAAA 63  
QY 37 GluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysala 56  
DB 64 GAGAAACAC--AAGCCACAGAAATCATCTTTAGATGAGAGAGGTGGCTCCCTCCAAAGGA 120  
QY 57 ValLysThrThrGly 61  
DB 121 TCCCAAACTACAGGA 135

RESULT 3  
US-08-560-398-3/c  
Sequence 3, Application US/08560398  
Patent No. 5907082  
GENERAL INFORMATION:  
APPLICANT: O'Neill, Sharman  
APPLICANT: Nadeau, Jeanette  
TITLE OF INVENTION: Ovule-Specific Gene Expression  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,398  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-063300US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1799 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 19..23  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 291..1571  
OTHER INFORMATION: /note= "clone O40 ovule-specific gene  
OTHER INFORMATION: encoding a cytochrome P450 monooxygenase  
OTHER INFORMATION: from pollen tubes of Phalaenopsis"  
US-08-560-398-3



EARLIER APPLICATION NUMBER: 60/048,900	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923	EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921	EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657	EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227	SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 243	LENGTH: 2271
TYPE: DNA	ORGANISM: Homo sapiens
FEATURE:	NAME/KEY: SITE
LOCATION: (553)	OTHER INFORMATION: n equals a,t,g, or c
FEATURE:	NAME/KEY: SITE
LOCATION: (2267)	OTHER INFORMATION: n equals a,t,g, or c
FEATURE:	NAME/KEY: SITE
LOCATION: (2271)	OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-243	Alignment Scores:



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Db 340 AGTACCAAGAAAAGTGG 357
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RESULT 6
US-09-107-532A-1899/c
; Sequence 1899, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...849
; SEQUENCE DESCRIPTION: SEQ ID NO: 1899:
US-09-107-532A-1899
Alignment Scores:
Pred. No.: 7.21 Length: 849
Score: 67.50 Matches: 24
Percent Similarity: 41.84% Conservative: 17
Best Local Similarity: 24.49% Mismatches: 29
Query Match: 14.61% Indels: 28
DB: 4 Gaps: 2
US-09-989-293A-377 (1-90) x US-09-107-532A-1899 (1-849)
Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn-ThrLeuGlu 27
::: ||| ::||
Db 527 ATCTTGATCTGCTGTTCTGAAATTTTGTGAGCAATCGAGCAATGCAATTCG 468
::: ||| ::||
Qy 27 uAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGlnSerSer-- 46
::: ||| ::||
Db 467 GAGACAGTATCCAGATTCATCAAGAGAAGCTTAAACCAACCAACCCAGCCTTCCAC 408
::: ||| ::||
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Qy 47 -----LeuGluAspSerValThrProThry 55
::: ||| ::||
Db 407 TGAAGGGCTCAATCGAAATTTGAGAAAGATAGATTGAAGAGCGCCAGCTGCCAACCA 348
::: ||| ::||
Qy 55 s-----AlaVallysthTh 60
::: ||| ::||
Db 347 ACAGCAAAACCTGCTGTCATAAAGGAATAACGGATGAAATCTTGAATAATTTGTTGAAT 288
::: ||| ::||
Qy 60 rGlyLysGlyIleVallysthGlyArgAsnLeuAspSerArgGlyLeuLeu 77
::: ||| ::||
Db 287 TGGTGAAGAGGCTTACATGGGAGAACTTAATCTACTGAACGTTTTTTA 236
::: ||| ::||
RESULT 7
US-09-242-690A-35
; Sequence 35, Application US/09242690A
; Patent No. 6284534
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/242,690A
; CURRENT FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02924
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Candida utilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(801)
US-09-242-690A-35
Alignment Scores:
Pred. No.: 7.78 Length: 804
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 3 Gaps: 2
US-09-989-293A-377 (1-90) x US-09-242-690A-35 (1-804)
Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
::: ||| ::||
Db 218 CTACTGTGGCTCCACTGTTGGAGCTTTCAAAGAGCACAAATTCCTCATCTTTGAGGACC 277
::: ||| ::||
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
::: ||| ::||
Db 278 GTAAGTTTGTGATATCGGCAACACCGTCACGCGGTGGTGGCGTTCAAGA 337
::: ||| ::||
Qy 47 LeuGluAspSerValThrProThrysAlaVallysthThrGlyLysGlyIleVally 66
::: ||| ::||
Db 338 TTGCGCAATGGGCGAGATATC-ACCAACGCCCGGTCACCGGTGAGTATCGTCAAG 396
::: ||| ::||
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
::: ||| ::||
Db 397 GGTTGAAGAGGCTCCACAGGAACACCGATGAGGAGGCTGTTGATGCTTGG 456
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Qy 80 GluAlaTrpGlyArgGly 85
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Db 457 GAGCTGAGCTCCCAAGGCGC 474
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RESULT 8
US-09-908-855-35
; Sequence 35, Application US/09908855
```

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; Patent No. 6610514
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; FILE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/908,855
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/242,690
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 35
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Candida utilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(801)
US-09-908-855-35

Alignment Scores:
Pred. No.: 7.78 Length: 804
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 4 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-908-855-35 (1-804)

Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 218 CTACTGGCTCCACTGTTGAGCTTCAAGAGACAAATTCCTCATCTTTGAGGACC 277
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSer 46
Db 278 GTAAGTTTGCTGATATCGGCACACCTCAGGCACAGTACGCCGGTGGTTCGAAGA 337
Qy 47 LeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGlyLeuValLys 66
Db 338 TTGCGCAATGGCGAGATATC-ACCAACGCCACCGTGTCCACCGTGCAGGTATCGTCAAG 396
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 397 GGGTTGAGGAGGCTGCACAGGAACCCAGGATGACGACAGAGGGCTGTGATGCTTGGC 456
Qy 80 GluAlaTrpGlyArgGly 85
Db 457 GAGCTGAGCTCCAAGGCC 474

RESULT 9
US-08-557-128-3
; Sequence 3, Application US/08557128
; Patent No. 5849524
; GENERAL INFORMATION:
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: MISA, No. 5849524ihiko
; TITLE OF INVENTION: TRANSFORMATION SYSTEMS FOR THE YEAST
; TITLE OF INVENTION: CANDIDA UTILIS AND THE EXPRESSION OF HETEROLOGOUS GENES
; TITLE OF INVENTION: THEREWITH
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Harder
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,128
; FILING DATE: 25-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP95/01005
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-129287
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-285823
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-135015
; FILING DATE: 25-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1259..2059
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1259..2059
; US-08-557-128-3

Alignment Scores:
Pred. No.: 39.2 Length: 2330
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 2 Gaps: 2

US-09-989-293A-377 (1-90) x US-08-557-128-3 (1-2330)

Qy 8 LeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 1476 CTACTGGCTCCACTGTTGAGCTTCAAGAGACAAATTCCTCATCTTTGAGGACC 1535
Qy 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSer 46
Db 1536 GTAAGTTTGCTGATATCGGCACACCTCAGGCACAGTACGCCGGTGGTTCGAAGA 1595
Qy 47 LeuGluAspSerValThrProThrLysAlaValLysThrThrGlyLysGlyLeuValLys 66
Db 1596 TTGCGCAATGGCGAGATATC-ACCAACGCCACCGTGTCCACCGTGCAGGTATCGTCAAG 1654
Qy 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 1655 GGGTTGAGGAGGCTGCACAGGAACCCAGGATGACGACAGAGGGCTGTGATGCTTGGC 1714
Qy 80 GluAlaTrpGlyArgGly 85
Db 1715 GAGCTGAGCTCCAAGGCC 1732
```

```
RESULT 10
US-09-242-690A-34
; Sequence 34, Application US/09242690A
; Patent No. 6284534
; ORGANISM: Candida utilis
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/242,690A
; CURRENT FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02924
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 2330
; TYPE: DNA
; ORGANISM: Candida utilis
US-09-242-690A-34

Alignment Scores:
Pred. No.: 39.2 Length: 2330
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 2 Gaps: 3

US-09-989-293A-377 (1-90) x US-09-242-690A-34 (1-2330)
QY 8 LeuLeuLeuValCysGluAlaIleTTPArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 1476 CTACTGTGGCTCCACTGTGGAGCTTTCAAAGAACACAAATTCCTCATCTTTGAGGACC 1535
QY 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
Db 1536 GTAAGTTTCTGATATCGGCACACCGTCACAGGCACAGTACGCCGTGGTGGTTCACAA 1595
QY 47 LeuGluAspSerValThrProThrLysAlaValLysThrGlyLysGlyIleValLys 66
Db 1596 TTGCGCAATGGCGAGATATC-ACCAACGCCACCGGTGCACCGGTGCAGGTATCGTCAAG 1654
QY 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 1655 GGGTTGAAGGAGGCTGCACAGGAACACCGATGACCAAGAGGCGCTGTGTGATGCTTGGC 1714
QY 80 GluAlaTTPGlyArgGly 85
Db 1715 GAGCTGAGTCCCAAGGGC 1732

RESULT 11
US-09-989-293A-377 (1-90) x US-09-242-690A-34 (1-2330)
QY 8 LeuLeuLeuValCysGluAlaIleTTPArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 1476 CTACTGTGGCTCCACTGTGGAGCTTTCAAAGAACACAAATTCCTCATCTTTGAGGACC 1535
QY 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
Db 1536 GTAAGTTTCTGATATCGGCACACCGTCACAGGCACAGTACGCCGTGGTGGTTCACAA 1595
QY 47 LeuGluAspSerValThrProThrLysAlaValLysThrGlyLysGlyIleValLys 66
Db 1596 TTGCGCAATGGCGAGATATC-ACCAACGCCACCGGTGCACCGGTGCAGGTATCGTCAAG 1654
QY 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 1655 GGGTTGAAGGAGGCTGCACAGGAACACCGATGACCAAGAGGCGCTGTGTGATGCTTGGC 1714
QY 80 GluAlaTTPGlyArgGly 85
Db 1715 GAGCTGAGTCCCAAGGGC 1732

RESULT 11
US-09-989-293A-377 (1-90) x US-09-242-690A-34 (1-2330)
; Sequence 34, Application US/09908855
; Patent No. 6610514
; ORGANISM: Pseudomonas aeruginosa
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MIURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/908,855
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/242,690
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
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; LENGTH: 2330
; TYPE: DNA
; ORGANISM: Candida utilis
US-09-989-293A-377 (1-90) x US-09-989-293A-377 (1-2330)

Alignment Scores:
Pred. No.: 39.2 Length: 2330
Score: 67.00 Matches: 28
Percent Similarity: 43.02% Conservative: 9
Best Local Similarity: 32.56% Mismatches: 41
Query Match: 14.50% Indels: 9
DB: 2 Gaps: 3

US-09-989-293A-377 (1-90) x US-09-989-293A-377 (1-2330)
QY 8 LeuLeuLeuValCysGluAlaIleTTPArgSerAsnSerGlySerAsnThrLeuGlu 27
Db 1476 CTACTGTGGCTCCACTGTGGAGCTTTCAAAGAACACAAATTCCTCATCTTTGAGGACC 1535
QY 28 AsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnPro---ThrGlnSerSer 46
Db 1536 GTAAGTTTCTGATATCGGCACACCGTCACAGGCACAGTACGCCGTGGTGGTTCACAA 1595
QY 47 LeuGluAspSerValThrProThrLysAlaValLysThrGlyLysGlyIleValLys 66
Db 1596 TTGCGCAATGGCGAGATATC-ACCAACGCCACCGGTGCACCGGTGCAGGTATCGTCAAG 1654
QY 67 Gly-----ArgAsnLeuAspSerArgGlyLeuLeuGlyAla 79
Db 1655 GGGTTGAAGGAGGCTGCACAGGAACACCGATGACCAAGAGGCGCTGTGTGATGCTTGGC 1714
QY 80 GluAlaTTPGlyArgGly 85
Db 1715 GAGCTGAGTCCCAAGGGC 1732

RESULT 12
US-09-252-991A-16320
; Sequence 16320, Application US/09252991A
; Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16320
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16320

Alignment Scores:
Pred. No.: 14 Length: 1065
Score: 66.50 Matches: 19
Percent Similarity: 41.89% Conservative: 12
Best Local Similarity: 25.68% Mismatches: 32
Query Match: 14.39% Indels: 11
DB: 2 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-252-991A-16320 (1-1065)
QY 15 AlaIleTTPArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34
Db 214 GCGCTGTGGACGGTTTCGACCGCGAGCAT-----GACCGCTGTATCGCTGCAACCC 267
QY 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54
Db 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54
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Db 268 TCGGCGAAGGTCCGACCGACCCCTGGCGAGCGCGAGAGTTTCATCGCTCGGACC 327  
 Qy 55 -----LysAlaValLysThrGlyLysGlyIleVal 65  
 Db 328 CGCGCGGACAGCGGTTGCCCTGGGCGATGACGACGCGGGTCTGCTCAGTGGCCTGGG 387  
 Qy 66 LysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAla 79  
 Db 388 CGCGGCGGCACTCGACTTCGAAGGCATCGCTCGCATGCC 429

RESULT 13  
 US-09-252-991A-15961/c  
 ; Sequence 15961, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 15961  
 ; TYPE: DNA  
 ; LENGTH: 1332  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-15961

Alignment Scores:  
 Pred. No.: 19.7 Length: 1332  
 Score: 66.50 Matches: 19  
 Percent Similarity: 41.89% Conservative: 12  
 Best Local Similarity: 25.68% Mismatches: 32  
 Query Match: 14.39% Indels: 11  
 DB: 4 Gaps: 2

US-09-989-293A-377 (1-90) x US-09-252-991A-15961 (1-1332)  
 Qy 15 AlaIleTyrArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArg 34  
 Db 885 GCCTGTGTGACGGTTTCCGACCGCGACGAT-----GACCGCTGTATCGCTCGCAACC 832  
 Qy 35 AsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrProThr 54  
 Db 831 TCGGCGAAGGTCCGACACGACCCCTGGCGCGCGAGGCGGAGTTTCATCGCTCGGACC 772  
 Qy 55 -----LysAlaValLysThrGlyLysGlyIleVal 65  
 Db 771 CGCGCGGACAGCGGTTGCCCTGGGCGATGACGACGCGGCTGTGGCTCAGTGGCCTGGTG 712  
 Qy 66 LysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAla 79  
 Db 711 CGCGGCGGCAACTCGACTTCGAAGGCATCGCTCGCATGCC 670

RESULT 14  
 US-09-621-976-3007/c  
 ; Sequence 3007, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pn  
 ; SEQ ID NO 3007

LENGTH: 548  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 127..453  
 US-09-621-976-3007  
 Alignment Scores:  
 Pred. No.: 7.02 Length: 548  
 Score: 65.50 Matches: 17  
 Percent Similarity: 54.39% Conservative: 14  
 Best Local Similarity: 29.82% Mismatches: 23  
 Query Match: 14.18% Indels: 3  
 DB: 4 Gaps: 1

US-09-989-293A-377 (1-90) x US-09-621-976-3007 (1-548)  
 Qy 4 PheLeuSerLeuLeuLeuValCysGluAlaIleTyrArgSerAsnSerGlySer 23  
 Db 504 TACCTCACCTCACATTGCTATTACGATTCAAGAGCTCCATAAACTGTCAAACTGGCAG 445  
 Qy 24 AsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThr 43  
 Db 444 AACACAGAGAACCATGGGCACCTTCTCCACAGGGTTTGAAGAACCATCAACGCTCTAGT 385  
 Qy 44 GlnSerSerLeuGlu-----AspSerValThrProThrLysAlaVal 57  
 Db 384 CCTGTTGACCTGGAAATGGTGGCAGGTGAAGTCTCTCCACAGCATGCCTTG 334

RESULT 15  
 US-09-134-000C-2940  
 ; Sequence 2940, Application US/09134000C  
 ; Patent No. 6617156  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; FILE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 032796-032  
 ; CURRENT APPLICATION NUMBER: US/09/134,000C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/055,778  
 ; PRIOR FILING DATE: 1997-08-15  
 ; NUMBER OF SEQ ID NOS: 6812  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2940  
 ; LENGTH: 744  
 ; TYPE: DNA  
 ; ORGANISM: Enterococcus faecalis  
 US-09-134-000C-2940

Alignment Scores:  
 Pred. No.: 11.2 Length: 744  
 Score: 65.50 Matches: 16  
 Percent Similarity: 44.23% Conservative: 7  
 Best Local Similarity: 30.77% Mismatches: 14  
 Query Match: 14.18% Indels: 15  
 DB: 4 Gaps: 1

US-09-989-293A-377 (1-90) x US-09-134-000C-2940 (1-744)  
 Qy 27 GluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGlnSerSer 46  
 Db 553 GAAAAAGGATACCTGATTAAAGAAAGGTACCGATTGGAATGCGCTACACAGAGTCA 612  
 Qy 47 Leu-----GluAspSerVal 51  
 Db 613 ATGGATCTCGAATTATTGAAGTGAAGAAAGACGATTTGCGACGTTCCGATGGTAGTGA 672  
 Qy 52 ThrProThrLysAlaValLysThrGlyLysGly 63  
 Db 673 AGTATCATGTAAGCGCTTAAGTTACTTGGGAAAGGT 708

Search completed: April 4, 2004, 09:55:54  
Job time : 97 secs

GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 4, 2004, 06:59:37 ; Search time 428 Seconds  
(without alignments)  
893.313 Million cell updates/sec

Title: US-09-989-293A-377  
Perfect score: 462  
Sequence: 1 MTFFLSLLILLVCEAIWRSN.....DSRGLILGAEAWGRGVKKNT 90

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: Geneseqn2002s:.\*  
7: Geneseqn2003as:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	712	5 AAC91481	Aac91481 Human PRO
2	462	100.0	713	3 AAZ65094	Aaz65094 Membrane-
3	462	100.0	713	3 AAC58634	Aac58634 Human PRO
4	462	100.0	713	4 AAS21480	Aas21480 Human cDN
5	462	100.0	713	5 AAF44240	Aaf44240 Human PRO
6	462	100.0	713	7 ABX77952	Abx77952 Human PRO
7	462	100.0	713	7 ABX80364	Abx80364 Novel hum
8	462	100.0	713	7 ACA69270	Ac69270 Human cDN

9	462	100.0	713	7 ACD24089	Ac24089 Novel hum
10	462	100.0	713	7 ABX90341	Abx90341 Human sec
11	462	100.0	713	7 ABX64187	Abx64187 cDNA enco
12	462	100.0	713	7 ACA67230	Ac67230 cDNA enco
13	462	100.0	713	7 ACA64409	Ac64409 Novel hum
14	462	100.0	713	7 ACA03839	Ac03839 cDNA enco
15	462	100.0	713	7 ABX89377	Abx89377 DNA enco
16	462	100.0	713	7 ABX80868	Abx80868 Human sec
17	462	100.0	713	7 ACD44377	Ac44377 cDNA enco
18	462	100.0	713	7 ACD42031	Ac42031 Human sec
19	462	100.0	713	7 ABX79548	Abx79548 Human sec
20	462	100.0	713	7 ACA93569	Ac93569 Novel hum
21	462	100.0	713	7 ABX81251	Abx81251 Novel hum
22	462	100.0	713	7 ACA04260	Ac04260 Human cDN
23	462	100.0	713	7 ACA93067	Ac93067 Novel hum
24	462	100.0	713	7 ABX17151	Abx17151 Human PRO
25	462	100.0	713	8 ACA68006	Ac68006 Novel hum
26	462	100.0	713	8 ACA88455	Ac88455 Human sec
27	462	100.0	713	8 ACD81962	Ac81962 cDNA enco
28	462	100.0	713	8 ADA45992	Ad45992 Novel hum
29	462	100.0	713	8 ADA76423	Ad76423 Human PRO
30	462	100.0	713	8 ADA19073	Ad19073 Human PRO
31	462	100.0	713	8 ADA61696	Ad61696 Homo sapi
32	462	100.0	713	8 ADB19481	Adb19481 Novel hum
33	462	100.0	713	8 ADB28022	Adb28022 cDNA enco
34	462	100.0	713	8 ADA86501	Ad86501 Novel hum
35	462	100.0	713	8 ADB16065	Adb16065 Human PRO
36	462	100.0	713	8 ADA37887	Ad37887 Human cDN
37	462	100.0	713	8 ADA47851	Ad47851 Human PRO
38	462	100.0	713	8 ADA21573	Ad21573 Human cDN
39	462	100.0	713	8 ADA10360	Ad10360 Human cDN
40	462	100.0	713	8 ADA67646	Ad67646 Human PRO
41	462	100.0	713	8 ADB30653	Adb30653 cDNA enco
42	462	100.0	713	8 ADA85949	Ad85949 Novel hum
43	462	100.0	713	8 ADA17904	Ad17904 cDNA enco
44	462	100.0	713	8 ADA97161	Ad97161 Human PRO
45	462	100.0	713	8 ADA79465	Ad79465 Human PRO

ALIGNMENTS

RESULT 1  
AAC91481  
ID AAC91481 standard; cDNA; 712 BP.

AC AAC91481;  
XX  
XX 21-MAR-2001 (first entry)  
XX Human PRO1159 cDNA.

XX Human; PRO; antiinflammatory; dermatological; antiarthritic;  
XX antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
XX antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
XX antiallergic; antiasthmatic; immune related disorder;  
XX hepatobiliary disease; autoimmune disease; allergy; ss.

OS Homo sapiens.

XX WO200073452-A2.

XX 07-DEC-2000.

XX 02-JUN-2000; 2000WO-US015264.

XX 02-JUN-1999; 99WO-US012252.

XX 20-JUL-1999; 99US-0144732P.

XX 20-JUL-1999; 99US-0144758P.

XX 28-JUL-1999; 99US-0146222P.

XX 01-SEP-1999; 99WO-US020111.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 29-OCT-1999; 99US-0162506P.



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PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 20-DEC-1999; 99WO-US030913.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
XX PA
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;
XX Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL,
XX Watanabe CK, Wood WI,
XX
XX WPI; 2001-025253/03.
XX P-PSDB; AAB50922.
XX
XX Thirty three nucleic acids encoding PRO polypeptides which are useful in
XX the diagnosis and treatment of immune related disorders, e.g. systemic
XX lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis
XX and diabetes mellitus.
XX
XX Claim 48; Fig 41; 218pp; English.
XX
XX The present sequence is one of thirty three nucleic acids encoding PRO
XX polypeptides. The PRO polypeptides, anti-PRO antibodies, agonists and
XX antagonists are useful for treating and diagnosing immune related
XX disorders such as systemic lupus erythematosus, rheumatoid arthritis,
XX osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
XX systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
XX syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
XX anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
XX immune-mediated renal disease, demyelinating diseases of the central and
XX peripheral nervous systems (such as multiple sclerosis, idiopathic
XX demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
XX inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such
XX as infectious, autoimmune chronic active hepatitis, primary biliary
XX cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
XX inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
XX disease, autoimmune or immune-mediated skin diseases (such as bullous
XX skin diseases, erythema multiforme, contact dermatitis, psoriasis),
XX allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
XX food hypersensitivity and urticaria), immunological diseases of the lung
XX (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
XX hypersensitivity pneumonitis), transplantation associated diseases
XX including graft rejection and graft-versus-host diseases
XX
XX Sequence 712 BP; 262 A; 105 C; 134 G; 211 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.03e-52 Length: 712
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

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US-09-989-293A-377 (1-90) x AAC91481 (1-712)

QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20  
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 Db 92 ATGACATTTTCTGTCTACTATTATTATTGGTATGTGAAGCTATTGGAGATCCCAAT 151  
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 QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40  
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 Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAAGAGAACACACAGT 211  
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 QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
 |||||  
 Db 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACA 271  
 |||||  
 QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80  
 |||||  
 Db 272 GGCAAGGGCAGTAGTTAPAGGACGGGAATCTTGACTCAGAGGGTTAAATCTTGGTCTGCTGAA 331  
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 QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
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 Db 332 GCTGGGGCAGGGGGTGTAAGAAAAACACT 361  
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RESULT 2  
 AAZ65094  
 ID AAZ65094 standard; cDNA; 713 BP.  
 XX  
 AC AAZ65094;  
 XX  
 DT 05-APR-2000 (first entry)  
 XX  
 DE Membrane-bound protein PRO1159 encoding cDNA.  
 XX  
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
 KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9963088-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99WO-US012252.  
 XX  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.  
 PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-0088328P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-0088212P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088655P.  
 PR 10-JUN-1998; 98US-0088722P.  
 PR 10-JUN-1998; 98US-0088730P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088738P.  
 PR 10-JUN-1998; 98US-0088740P.  
 PR 10-JUN-1998; 98US-0088741P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
 PR 10-JUN-1998; 98US-0088811P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088825P.  
 PR 10-JUN-1998; 98US-0088828P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088861P.

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PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 16-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089807P.
PR 18-JUN-1998; 98US-0089808P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
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PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095923P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.

PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 31-AUG-1998; 98US-0098014P.
PR 16-SEP-1998; 98US-0098525P.
PR 12-JAN-1999; 99US-0115565P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX WPI; 2000-072883/06.
XX P-PSDB; AAY66748.
XX
XX Membrane-bound proteins and related nucleotide sequences.
XX
XX Claim 2; Fig 271; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences will
XX also be useful for the preparation of PRO polypeptides, especially by
XX recombinant techniques
XX
XX SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-989-293A-377 (1-90) x AAZ65094 (1-713)

```

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Qy 1 MetThrPheLeuSerLeuLeuLeuLeuValCysGluAlaIleTTPArgSerAsn 20
Db 92 ATGACATTTTCTGCTCACTATTATTATTTGGTATGTGAAGCTATTGTGAGATCCAAT 151
Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCACACACTTGGAGATGGCTACTTCTTATCAAGAAATAAGAGACACACAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGACACAGTGTGACTCTTACCAAGCTGTCAAAACCACA 271
Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GCGAAGGGCATAGTTAAAGACGCGAATCTTGACTCAAGAGGGTTAATTTCTTGGTCTGAA 331
Qy 81 AlaTTPGlyArgGlyValLysLysAsnThr 90
Db 332 GCTGGGCGAGGGGTAAAGAAACACT 361
RESULT 3
AAC58634
ID AAC58634 standard; cDNA; 713 BP.
XX
AC AAC58634;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1159 protein UNQ589 encoding cDNA SEQ ID NO:272.
XX
KW Human; immune related disease; diagnosis; antinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; anti allergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW Graft rejection; graft-versus-host-disease; ss.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0145775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
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PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI: 2000-572271/53.
DR P-PSDB; AAB33469.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 23; Fig 111; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases, inflammatory bowel
CC peripheral nervous systems, hepatobiliary diseases, Whipple's disease,
CC disease, gluten-sensitive enteropathy and allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-989-293A-377 (1-90) x AAC58634 (1-713)
Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTTPArgSerAsn 20
Db 92 ATGACATTTTCTGCTCACTATTATTATTTGGTATGTGAAGCTATTGTGAGATCCAAT 151
Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
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Db 152 TCAGGAGCAACATCTGGAGATGGCTACTTCTATCAAGAAATAAGAGAACACAGT 211  
 Qy 41 GlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
 Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACA 271  
 Qy 61 GlyLysGlyLysValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyValaGlu 80  
 Db 272 GGCAGGGGCTAGTTAAGGACCGGAATCTTGACTCAAGAGGGTTAATCTTGGTGTCTGAA 331  
 Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
 Db 332 GCCTGGGCGAGGGGTGTAAAGAAAAACACT 361  
 RESULT 4  
 ID AAS21480 standard; cDNA; 713 BP.  
 XX  
 AC AAS21480;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human cDNA sequence encoding for PRO1159 polypeptide.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIa; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US032678.  
 XX  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 09-DEC-1999; 99US-0170262P.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 03-MAR-2000; 2000US-018702P.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR P-PSDB; AAU12408.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
 PT breast, prostate, cervical.  
 XX  
 PS Claim 3; Fig 473; 813pp; English.  
 XX  
 CC AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful to detect other PRO  
 CC polypeptides, to link bioactive molecules to cells expressing PRO  
 CC polypeptides, to modulate biological activities of cells expressing PRO  
 CC polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample. Some  
 CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy  
 XX  
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6,04e-52 Length: 713  
 Score: 462.00 Matches: 90  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-989-293A-377 (1-90) x AAS21480 (1-713)  
 Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20  
 Db 92 ATGACATTTTTTCTGTCTATTTATTTATTTGGTATGGAAGCTATTTGGAGATCCAT 151  
 Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40  
 Db 152 TCAGGAGCAACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACA 211  
 Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
 Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACA 271  
 Qy 61 GlyLysGlyLysValLysGlyArgAsnLeuAspSerArgGlyLeuLeuLeuGlyValaGlu 80  
 Db 272 GGCAGGGGCTAGTTAAGGACCGGAATCTTGACTCAAGAGGGTTAATCTTGGTGTCTGAA 331  
 Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
 Db 332 GCCTGGGCGAGGGGTGTAAAGAAAAACACT 361

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RESULT 5
AAF44240
ID AAF44240 standard; cDNA; 713 BP.
XX
AC AAF44240;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1159 (UNQ589) nucleotide sequence SEQ ID NO:376.
XX
DE Human; secreted and transmembrane protein; PRO; cytosstatic; cell death;
XX
KW cancer; chromosomal mapping; Gene mapping; tissue typing;
XX
KW diagnostic assay; ss.
XX
OS Homo sapiens.
XX
FN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
XX
PR 23-JUN-1999; 99US-0141037P.
XX
PR 07-JUL-1999; 99US-0143048P.
XX
PR 26-JUL-1999; 99US-0144758P.
XX
PR 26-JUL-1999; 99US-0145698P.
XX
PR 28-JUL-1999; 99US-0146222P.
XX
PR 17-AUG-1999; 99US-0149396P.
XX
PR 15-SEP-1999; 99WO-US021090.
XX
PR 15-SEP-1999; 99WO-US021547.
XX
PR 08-OCT-1999; 99US-0153663P.
XX
PR 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1999; 99WO-US028301.
XX
PR 16-DEC-1999; 99WO-US030095.
XX
PR 20-DEC-1999; 99WO-US030911.
XX
PR 05-JAN-2000; 2000WO-US000219.
XX
PR 06-JAN-2000; 2000WO-US000376.
XX
PR 11-FEB-2000; 2000WO-US003565.
XX
PR 18-FEB-2000; 2000WO-US004341.
XX
PR 22-FEB-2000; 2000WO-US004414.
XX
PR 24-FEB-2000; 2000WO-US004914.
XX
PR 24-FEB-2000; 2000WO-US005004.
XX
PR 02-MAR-2000; 2000WO-US005841.
XX
PR 15-MAR-2000; 2000WO-US005884.
XX
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart IA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
XX
DR P-PSDB; AAB65271.
XX
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
XX molecules such as toxins, radiolabels or antibodies, to specific cells,
XX to cause targeted cell death.
XX
XX Claim 2; Fig 271; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytosstatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
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CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-989-293A-377 (1-90) x AAF44240 (1-713)
QY 1 MetThrPhePheLeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
Db 92 ATGACATTTTTCGTCTCACTATTATTATTGTTGTTGTAAGCTATTGAGATCCAAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAGAAATAAAGAGAACACAGT 211
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACAAATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCA 271
QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GGCAGGGGCATAGTTAAAGGACCGAATCTTGACTCAGAGGGTTAAATCTTGGTGTGAA 331
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
Db 332 GCCTGGGGCAGGGGTGTTAAGAAAAACACT 361

RESULT 6
ABX77952
ID ABX77952 standard; cDNA; 713 BP.
XX
AC ABX77952;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polynucleotide #118.
XX
XX Human; PRO; gene; ss; cytosstatic; tumour; cancer; breast; lung; stomach;
XX liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
XX antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
XX
XX US2003027163-A1.
XX
XX 06-FEB-2003.
XX
XX 15-NOV-2001; 2001US-00997666.
XX
XX 16-JUN-1997; 97US-0049787P.
XX
XX 17-OCT-1997; 97US-0062250P.
XX
XX 05-NOV-1997; 97WO-US020069.
XX
XX 12-NOV-1997; 97US-0065186P.
XX
XX 13-NOV-1997; 97US-0065311P.
XX
XX 24-NOV-1997; 97US-0066770P.
XX
XX 25-FEB-1998; 98US-0075945P.
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XX 20-MAR-1998; 98US-0078910P.
XX
XX 28-APR-1998; 98US-0083322P.
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XX 07-MAY-1998; 98US-0084600P.
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XX 28-MAY-1998; 98US-0087106P.
XX
XX 02-JUN-1998; 98US-0087607P.
XX
XX 02-JUN-1998; 98US-0087609P.
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06-JAN-2000; 2000WO-US000376.  
 11-FEB-2000; 2000WO-US003565.  
 18-FEB-2000; 2000WO-US004341.  
 22-FEB-2000; 2000WO-US004414.  
 24-FEB-2000; 2000WO-US004914.  
 24-FEB-2000; 2000WO-US005004.  
 02-MAR-2000; 2000WO-US005841.  
 10-MAR-2000; 2000WO-US006319.  
 15-MAR-2000; 2000WO-US006884.  
 20-MAR-2000; 2000WO-US007377.  
 30-MAR-2000; 2000WO-US008439.  
 15-MAY-2000; 2000WO-US013358.  
 17-MAY-2000; 2000WO-US013705.  
 22-MAY-2000; 2000WO-US014042.  
 30-MAY-2000; 2000WO-US014941.  
 02-JUN-2000; 2000WO-US015264.  
 28-JUL-2000; 2000WO-US020710.  
 11-AUG-2000; 2000WO-US022031.  
 23-AUG-2000; 2000WO-US023522.  
 24-AUG-2000; 2000WO-US023328.  
 08-NOV-2000; 2000WO-US030952.  
 01-DEC-2000; 2000WO-US032678.  
 28-FEB-2001; 2001WO-US0006520.  
 01-JUN-2001; 2001WO-US017800.  
 20-JUN-2001; 2001WO-US019692.  
 23-JUN-2001; 2001WO-US021066.  
 09-JUL-2001; 2001WO-US021735.  
 28-AUG-2001; 2001US-00941992.  
 (GETH ) GENENTECH INC.  
 Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;  
 Ferrara N, Fong S, Gerber H, Gerecht ME, Goddard A, Godowski PU;  
 Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J, Paoni NF;  
 Roy MA, Stewart TA, Tumas D, Watanabe CX, Williams PM, Wood WI;  
 Zhang Z;  
 WPI; 2003-247083/24.  
 P-PSDB; ABUS9165.  
 Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO184, PRO1346  
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 are therapeutically useful for enhancing immune response and in cancer  
 treatments.  
 Claim 2; Fig 273; 648pp; English.  
 The invention describes an isolated human PRO polypeptide. The PRO  
 polypeptides are useful in detecting PRO polypeptides in a sample, in  
 linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 in modulating at least one biological activity of a cell expressing a PRO  
 polypeptide. PRO132 stimulates hypertrophy of neonatal heart and is thus  
 useful for treating cardiac insufficiency disorders. PRO154 and PRO186  
 stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO184, PRO1126,  
 PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 useful for treating conditions or disorders where angiogenesis would be  
 beneficial, e.g. wound healing and antagonist of this polypeptide are  
 useful for treating cancerous tumours. PRO812 inhibits vascular  
 endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 cells and is thus useful for inhibiting endothelial cell growth in  
 mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 PRO1068, PRO184, PRO1346 and PRO1375 stimulate proliferation of  
 stimulated T-lymphocytes and are therapeutically useful for enhancing  
 immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 rod photoreceptor cells) and therefore are useful for treating retinal  
 disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 and therefore are useful for treating kidney disorders associated with  
 decreased mesangial cell function such as Berger disease or other  
 nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the

CC proliferation and/or redifferentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This sequence  
 CC represents a novel human PRO protein polynucleotide  
 XX  
 SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:  
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US-09-989-293A-377 (1-90) x ABX80364 (1-713)

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 DB 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACCA 271

QY 61 GlyLysGlyLysValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGlu 80  
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QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90

DB 332 GCCTGGGGCAGGGGTGTAAAGAAACACT 361

RESULT 8

ACA69270

ID ACA69270 standard; cDNA; 713 BP.

XX ACA69270;

XX 26-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1159.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;  
 KW cardiac insufficiency disorders; angiogenesis; wound healing;  
 KW cancerous tumour; immune response; retinal disorder; sight loss;  
 KW retinitis pigmentosa; age-related macular degeneration; AMD;  
 KW kidney disease; Berger disease; nephropathy; dermatitis; herpeticiformis;  
 KW Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

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XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

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XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087507P.



Mon Apr 5 12:02:00 2004

us-09-989-293a-377.rng

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PR	05-JAN-2000;	98US-0158663P.

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US-09-989-293A-377 (1-90) x ACA69270 (1-713)</									

RESULT 9	
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XX	26-AUG-2003 (first entry)
XX	
XX	Novel human secreted and transmembrane protein PRO1159 cDNA.
DE	
XX	Human, secreted and transmembrane protein; PRO; antiinflammatory;
XX	antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW	TNF-alpha release; cell proliferation; cell differentiation;
KW	gene expression modulator; proteoglycan release; cytokine release;
KW	tumour; inflammatory disease; organ failure; atherosclerosis;
KW	cardiac injury; infertility; birth defect; premature aging; AIDS;
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;
KW	chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW	bioreactor; tissue typing; gene; ss.
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XX	Homo sapiens.
XX	
XX	

OS



XX 26-FEB-2003 (first entry)  
XX cDNA encoding human PRO1159 polypeptide.  
DE Human; PRO polypeptide; secreted protein; transmembrane protein;  
XX genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
XX Homo sapiens.  
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XX US2002103125-A1.  
XX 01-AUG-2002.  
XX 20-NOV-2001; 2001US-00989731.  
XX 16-JUN-1997; 97US-0049787P.  
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PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001WO-US021992.  
XX (GETH ) GENENTECH LTD.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; Zhang Z;  
XX WPI: 2003-102117/09.  
DR P-PSDB; ABU13977.  
XX  
PT Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.  
XX  
PS Claim 2; Fig 271; 649pp; English.  
XX  
CC The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/patents/entry.html

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XX SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
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Qy 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTyrArgSerAsn 20
Db 92 ATGACATTTTCTGCTACTATTATTATGTGTGATGTGAAGCTATTTGGAGATCCAAT 151
Qy 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAGCACACATTTGGAGATGGCTACTTCTATCAAGATATAAGAGACACACAGT 211
Qy 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACATCATCTTTAGAGACAGTGTGACTCTCCTACCAAGGCTGTCAAAACACCA 271
Qy 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GCGAAGGGCATAGTTAAAGGACGGAACTTCTGACTCAAGAGGGTTAANTCTTGGTGCTGAA 331
Qy 81 AlaTrpGlyArgGlyValLysLysAsnThr 90
Db 332 GCCTGGGCGACGGGTGTAAAGAAACAACT 361
RESULT 12
ACA67230
ID ACA67230 standard; cDNA; 713 BP.
XX AC ACA67230;
XX DT 23-JUN-2003 (first entry)
XX DE cDNA encoding human PRO polypeptide #237.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
XX KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
XX KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
XX KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
XX KW antidiabetic; anorectic; vulnerable; antiarthritic; osteopathic;
XX KW antirheumatic; auditory; cerebroprotective; angiogenic; gene; ss.
OS Homo sapiens.
XX XX
XX FN US2003004311-Al.
XX PD
XX PF 19-DEC-2001; 2001US-00028072.
XX PR 18-JUN-1997; 97US-0049911P.
XX PR 26-AUG-1997; 97US-0056974P.
XX PR 17-SEP-1997; 97US-0059113P.
XX PR 17-SEP-1997; 97US-0059115P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 17-SEP-1997; 97US-0059122P.
XX PR 17-SEP-1997; 97US-0059184P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 19-SEP-1997; 97US-0059352P.
XX PR 19-SEP-1997; 97US-0059588P.
XX PR 24-SEP-1997; 97US-0059936P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079234P.
PR 27-MAR-1998; 98US-0079563P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUN-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028314.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
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PR 30-DEC-1999; 99WO-US0311243.
PR 30-DEC-1999; 99WO-US0311274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
XX
XX WPI; 2003-352836/33.
XX P-PSDB; ABU81106.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
XX arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
XX heart attack.
XX
XX Claim 2; Fig 473; 643pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the treatment of diabetes, bone and/or cartilage disorders
XX (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
XX hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
XX (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
XX assays for PRO, by detecting its expression in specific cells, tissues or
XX serum, and for affinity purification of PRO from recombinant cell culture
XX or natural sources. ACA6994-ACA67268 represent cDNA sequences encoding
XX the human PRO polypeptides of the invention. Note: The sequence data for
XX this patent was obtained in electronic format directly from the USPTO web
XX site at seqdata.uspto.gov/psipds/IDEntry.html
XX
XX SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-52 Length: 713
Score: 462.00 Matches: 90
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ACA67230 (1-713)

QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20
Db 92 ATGACATTTTCTGTCACTATTATTATTATTGTTGGTAAGTCTATTGGAGATCCAT 151
QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40
Db 152 TCAGGAAGCAACACATTTGGAGATGGCTACTTTCTATCAAGAAATAAGAGAACACACAGT 211
QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
Db 212 CAACCCACACAAATCATCTTTTAGAAGACAGTGTGACTCTTACCACAACTGTCAAAACCA 271
QY 61 GlyLysGlyTleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80
Db 272 GGCAGGGCNCATGTTAAGACCGAATCTTGACTCAGAGGGTTAATCTTGTGTGTGAA 331
QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90

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Db 332 GCCTGGGCAGGGGTGTAAGAAACACT 361
RESULT 13
ACA64409
ID ACA64409 standard; cDNA; 713 BP.
XX
XX ACA64409;
XX
XX 17-JUN-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO1159 cDNA.
XX
XX Human; secreted and transmembrane protein; cytostatic; anti-HIV;
XX virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
XX PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
XX cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
XX lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
XX drug screening; gene; ss.
XX
XX Homo sapiens.
XX
XX OS US2003003531-A1.
XX
XX PD 02-JAN-2003.
XX
XX PF 19-NOV-2001; 2001US-00989734.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0065770P.
XX 25-FEB-1998; 98US-0075945P.
XX 28-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088026P.
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XX 04-JUN-1998; 98US-0088029P.
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XX 05-JUN-1998; 98US-0088167P.
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XX 09-JUN-1998; 98US-0088655P.
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XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088824P.
XX 11-JUN-1998; 98US-0088826P.
XX 11-JUN-1998; 98US-0088858P.
XX 11-JUN-1998; 98US-0088861P.
XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089532P.
XX 17-JUN-1998; 98US-0089538P.
XX 17-JUN-1998; 98US-0089598P.
XX 17-JUN-1998; 98US-0089599P.

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PR 17-JUN-1998; 98US-0089600P.  
 PR 17-JUN-1998; 98US-0089653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089907P.  
 PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 17-SEP-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US013252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005641.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 PR (GETH ) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski FJ;  
 PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX WPI; 2003-352829/33.  
 DR P-PSDB; ABU72562.  
 XX  
 XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
 PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
 PT disease.  
 XX  
 PS Claim 1; Fig 271; 663pp; English.  
 XX  
 CC The invention describes a new isolated nucleic acid molecule comprising  
 CC the full length coding sequence of the DNA deposited with the American  
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,  
 CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA  
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These

CC are particularly useful for detecting or treating e.g. malignancies or  
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
 CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
 CC disease in mammals. The PRO polypeptides are useful in drug screening,  
 CC particularly as targets for therapeutic intervention in these diseases,  
 CC and in the diagnostic determination of the presence of these diseases.  
 CC The PRO polypeptides are also useful as molecular weight markers, or for  
 CC chromosome identification. The PRO genes are useful as hybridisation  
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
 CC The PRO genes may also be used in gene therapy, particularly for  
 CC replacing a defective gene. This sequence encodes a novel human secreted  
 CC and transmembrane PRO polypeptide

SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 6,04e-52 Length: 713  
 Score: 462.00 Matches: 90  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US-09-989-293A-377 (1-90) x ACA64409 (1-713)

QY 1 MetThrPhePheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsn 20  
 Db 92 ATGACATTTTTCGTCACATATATATTGTTGGTATGTGAGCTATTGGAGATCCAAT 151  
 QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40  
 Db 152 TCAGGAAGCAACACATTTGAGATGGCTACTTTCTATCAAGAAATAAGAGAACACACAGT 211  
 QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
 Db 212 CAACCCACACATCATCTTTAGAAGACAGTGTGACTCTTACCACAAAGCTGTCAAAACACCA 271  
 QY 61 GlyLysGlyIleValLysGlyArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80  
 Db 272 GGCAGGGCATGTTAAAGACCGAATCTTGACTCAAGAGGGTTAATCTTGTGCTGAA 331  
 QY 81 AlaTrpGlyArgGlyValLysLysAsnThr 90  
 Db 332 GCCTGGGGCAGGGGTGTAAAGAAAAACACT 361

#### RESULT 14

ACA03839  
 ID ACA03839 standard; cDNA; 713 BP.

XX ACA03839;

XX 23-MAY-2003 (first entry)

XX cDNA encoding human PRO polypeptide #237.

XX Human; PRO polypeptide; secreted and transmembrane protein;  
 XX tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 XX differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;  
 XX ss.

XX Homo sapiens.

XX US2003036180-A1.

XX 20-FEB-2003.

XX 09-MAY-2002; 2002US-00143114.

XX 31-MAR-1997; 97WO-US005230.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.



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PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
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PR 15-SEP-1999; 99WO-US021547.
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PR 01-DEC-1999; 99WO-US028634.
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PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US030873.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US047259.
PR 28-FEB-2001; 2001WO-US034956.
PR 28-FEB-2001; 2001WO-US078648.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
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PR 10-MAY-2001; 2001US-00854208.
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PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 29-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
DR P-ESDB; ABU66806.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
therapy, in chromosome and gene mapping, as chromosome markers, in tissue
typing, and in chromosome identification.
XX Claim 2; Fig 473; 660pp; English.
XX The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
bioactive molecules to cells expressing PRO polypeptides, and for
biological activities of cells expressing PRO polypeptides, and for
identifying agonists or antagonists. The PRO polypeptides are useful for
stimulating the release of tumour necrosis factor (TNF)-alpha from
human blood, for stimulating the proliferation or differentiation of
chondrocytes, and detecting the presence of tumours. The polynucleotide
sequences encoding PRO polypeptides are useful as hybridisation probes,
in chromosome and gene mapping, in the generation of antisense RNA and
DNA, in the preparation of PRO polypeptides, for generating transgenic
animals or knockout animals, for the genetic analysis of individuals with
genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
encoding the human PRO polypeptides of the invention. Note: The sequence
data for this patent was obtained in electronic format directly from the
USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
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SQ Sequence 713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;

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DT 13-MAY-2003 (first entry)  
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KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpetic keratitis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.  
XX  
OS Homo sapiens.  
XX  
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XX US2003017563-A1.  
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XX 23-JAN-2003.  
XX  
XX 07-MAY-2002; 2002US-00140808.  
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XX 31-MAR-1997; 97WO-US005230.  
XX 12-JUN-1998; 98WO-US012456.  
XX 14-JUL-1998; 98WO-US014552.  
XX 28-AUG-1998; 98WO-US017888.  
XX 10-SEP-1998; 98WO-US018824.  
XX 14-SEP-1998; 98WO-US019094.  
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XX 17-SEP-1998; 98WO-US019330.  
XX 17-SEP-1998; 98WO-US019437.  
XX 07-OCT-1998; 98WO-US021141.  
XX 29-OCT-1998; 98WO-US022891.  
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XX 20-NOV-1998; 98WO-US024855.  
XX 01-DEC-1998; 98WO-US025108.  
XX 05-JAN-1999; 99WO-US000106.  
XX 08-MAR-1999; 99WO-US005028.  
XX 10-MAR-1999; 99WO-US005190.  
XX 20-APR-1999; 99WO-US008615.  
XX 14-MAY-1999; 99WO-US010733.  
XX 02-JUN-1999; 99WO-US012252.  
XX 01-SEP-1999; 99WO-US020111.  
XX 08-SEP-1999; 99WO-US020594.  
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XX 29-NOV-1999; 99WO-US028214.  
XX 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
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PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
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PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 11-FEB-2000; 2000WO-US000376.  
PR 18-FEB-2000; 2000WO-US000365.  
PR 18-FEB-2000; 2000WO-US000431.  
PR 18-FEB-2000; 2000WO-US000432.  
PR 22-FEB-2000; 2000WO-US000441.  
PR 24-FEB-2000; 2000WO-US000491.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 10-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 20-MAR-2000; 2000WO-US006884.  
PR 21-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US0008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 28-FEB-2001; 2001US-00796498.  
PR 01-MAR-2001; 2001WO-US006520.  
PR 09-MAR-2001; 2001WO-US006566.  
PR 14-MAR-2001; 2001US-00802706.  
PR 22-MAR-2001; 2001US-00808689.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882536.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 16-AUG-2001; 2001US-00927796.  
PR 19-DEC-2001; 2001US-00931836.  
XX  
XX (GETH ) GENENTECH INC.  
XX



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 4, 2004, 07:01:32 ; Search time 3358 Seconds  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 28: em\_un.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	462	100.0	713	6	AX464340	Sequence
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10	247.5	53.6	744	9	AF400595	Homo sapi
11	247.5	53.6	744	9	AY026769	Homo sapi
12	247.5	53.6	787	9	AF400601	Homo sapi
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20	208	45.0	221471	2	AC138620	Mus muscu
21	184.5	39.9	273867	2	AC112033	Rattus no
22	143.5	31.1	2298	6	BD056525	Unigue de
23	143.5	31.1	2298	10	AF262985	Mus muscu
24	139.5	30.2	528	6	BD056528	Unigue de
25	136.5	29.5	1329	10	BC027742	Mus muscu
26	122	26.4	85	6	AX912349	Sequence
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29	86.5	18.7	220557	2	AC111741	Rattus no
30	85	18.4	237031	2	AC128368	Rattus no
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37	81	17.5	254951	2	AC122999	Rattus no
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41	80	17.3	163309	2	AC116727	Mus muscu
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DEFINITION Sequence 376 from Patent WO0073454.
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VERSION AX403489.1 GI:21436980
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnovers,L., Eaton,D.,
Ferrara,N., Gerber,H., Geritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kijavini,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 376 07-DEC-2000;
Genentech Inc. (US)
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,  
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,  
Wood, W.L. and Zhang, Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 473 07-JUN-2001;  
Genentech Inc. (US)  
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QY 61 GlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLysLeuGlyAlaGlu 80  
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Db 332 GCCTGGGGCAGGGGTGTAAAGAAAAACACT 361

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DEFINITION Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.  
ACCESSION AY358685  
VERSION AY358685.1 GI:37182491  
KEYWORDS FLI CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 713)  
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,  
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,  
Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E.,  
Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S.,  
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Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,  
Goddard, A., Wood, W.L. and Godowski, P.  
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)  
PUBMED 12975309  
REFERENCE 2 (bases 1 to 713)  
AUTHORS Clark, H.F.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 9

US-09-989-293A-377 (1-90) x AY358685 (1-713)

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QY 21 SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSer 40  
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Db 152 TCAGGAAGCAACACATGAGAAATGGCTACTTTCTATCAAGAAATAAAGAACACCACT 211  
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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
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US-09-989-293A-377 (1-90) x AC024224 (1-165414)
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QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60
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QY 61 GlyLysGlyLleValLysGlyArgAsnLeuAspSerArgGlyLeuLleuGluAlaGlu 80
DB 117148 GGCNAAGGGCANTAGTTAAAGGACGGAATCTTGACTCAGAGGGTTAATTTCTGGTCTGAA 117089
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DB 117088 GCTGGGGCAGGGGTGTAAGAAACACT 117059

RESULT 7
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DEFINITION Homo sapiens clone RP11-13CL3, RP11-656E20, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
AC006510 AC006514
VERSION AC006510.8 GI:10122018
HTG: HTGS PHASE1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.  
and Gibbs R.  
Direct Submission  
Unpublished  
2 (bases 1 to 240864)  
Worley,K.C.  
Direct Submission  
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor  
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 14, 2000 this sequence version replaced gi:10086352.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: J-33  
Center clone name: RP11-13C13, RP11-656E20  
----- Summary Statistics  
Sequencing vector: Plasmid; M77789  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye; 23% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 71594 bases at least Q40  
Consensus quality: 93014 bases at least Q30  
Consensus quality: 110702 bases at least Q20  
Estimated insert size: 229041; sum-of-contigs estimation  
Estimated insert size: 331000; agarose-fp estimation  
Quality coverage: 0.6x in Q20 bases; agarose-fp estimation  
Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation  
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NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 16 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

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194803 194902: gap of unknown length  
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US-09-989-293A-377 (1-90) x AC006510 (1-240864)

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QY 60 Thr-GlyLysGlyLleValLys-GlyArgAsnLeuAspSer-ArgGlyLleuLleuGly 78  
Db 211479 ACCAGCAAGGCATAGTTTAAACAGACGGAATCTTGACTCAAGAGGGTTAATCTTGT 211420  
QY 79 AlaGluAlaIleTTPArgGlyValLysLysAsnThr 90  
Db 211419 GCTGAGCTGGGGCAGGGGTGTAAAGAAACACT 211384

## RESULT 8

AF400597

LOCUS

DEFINITION

AF400597

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

gene

CDS

AF400597

Homo sapiens beta-glucan receptor isoform C (BGR) mRNA, complete cds, alternatively spliced.

625 bp mRNA linear PRI 19-NOV-2001

AF400597.1 GI:15936703

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Willment, J.A., Gordon, S. and Brown, G.D.

Characterization of the human beta-glucan receptor and its

alternatively spliced isoforms

J. Biol. Chem. 276 (47), 43818-43823 (2001)

21570237

11567029

2 (bases 1 to 625)

Willment, J.A., Gordon, S. and Brown, G.D.

Direct Submission

Submitted (18-JUL-2001) Sir William Dunn School of Pathology,

Oxford University, South Parks Road, Oxford OX1 3RE, UK

Location/Qualifiers

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US-09-989-293A-377 (1-90) x AF400597 (1-625)

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Db 217 AATTCAGGAGCAACACATTCATCTTTAGAGACAGTGTGACTCTCTACCAAGAGTGTCAAAACC 276
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## RESULT 9

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DEFINITION Novel membrane protein and DNA thereof.
ACCESSION E21012
VERSION E21012.1 GI:13023572
KEYWORDS JP 1999001497-A/2.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 741)
AUTHORS Shuji.H., Shoji.F., Kazunori.N. and Yasushi.A.
TITLE Novel membrane protein and DNA thereof
JOURNAL Patent: JP 1999001497-A 2 06-JAN-1999;
COMMENT TAKEDA CHEM IND LTD
OS Unidentified
PN JP 1999001497-A/2
PD 06-JAN-1999
PF 13-JUN-1997 JP 1997156376
PR
PI SHUJI HINUMA, SHOJI FUKUZUMI, KAZUNORI NISHI, YASUSHI ARAVA PC
C07K14/47, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/00, PC
A61K39/395,
PC A61K48/00, C07K16/28, C12N1/21, C12N15/09, C12P21/02, C12Q1/68, PC
G01N33/53//
PC (C12N1/21, C12R1:19), (C12N15/09, C12R1:91), A61K37/02, A61K37/02,
PC A61K37/02,
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CC Topology: Linear;
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## ORIGIN

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Query Match: 53.57% Indels: 5
DB: 6 Gaps: 1
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US-09-989-293A-377 (1-90) x E21012 (1-741)

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QY 40 SerGlnProThrGlnSerLeuGluAAspSerValThrProThrLysAlaValLysThr 59
Db 277 AGTCAACCCACACATCATCTTTTGAAGACAGTGTGACTCTCTACCAAGAGTGTCAAAACC 336
QY 60 ThrGly 61
Db 337 ACAGGG 342
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## RESULT 10

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DEFINITION Homo sapiens beta-glucan receptor isoform A (BGR) mRNA, complete
cds, alternatively spliced.
ACCESSION AF400595
VERSION AF400595.1 GI:15986699
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Characterization of the human beta -glucan receptor and its
alternatively spliced isoforms
JOURNAL J. Biol. Chem. 276 (47), 43818-43823 (2001)
MEDLINE 21570237
PUBMED 11567029
REFERENCE 2 (bases 1 to 744)
AUTHORS Willment,J.A., Gordon,S. and Brown,G.D.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2001) Sir William Dunn School of Pathology,
Oxford University, South Parks Road, Oxford OX1 3RE, UK
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## ORIGIN

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 Score: 247.50  
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 Best Local Similarity: 80.65% Mismatches: 3  
 Query Match: 53.57% Indels: 5  
 DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x AF400595 (1-744)

QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19  
 Db 157 CTATGCTTGGTAATACCTGGTGTCTGGTACCATGGCTATTGGAGATCC 216  
 QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39  
 Db 217 AATTCAAGGAAGCAACATCGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAC 276  
 QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59  
 Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAACC 336  
 QY 60 ThrGly 61  
 Db 337 ACAGGG 342

## RESULT 11

AY026769 744 bp mRNA linear PRI 05-OCT-2001  
 LOCUS  
 DEFINITION Homo sapiens lectin-like receptor 1 (DECTIN1) mRNA, complete cds.

ACCESSION AY026769  
 VERSION AY026769.2 GI:15967096

KEYWORDS  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 744)  
 Hernandez-Falcon, P., Arce, I., Roda-Navarro, P. and Fernandez-Ruiz, E.

Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene  
 expressed on dendritic cells

Immunogenetics 53 (4), 288-295 (2001)

21383615

PUBMED 11491532

2 (bases 1 to 744)

Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.

## AUTHORS

## TITLE

Submitted (01-FEB-2001) Biologia Molecular, Hospital de la

Princesa, Diego de Leon 62, Madrid 28006, Spain

3 (bases 1 to 744)

Herranz-Falcon, P., Arce, I. and Fernandez-Ruiz, E.

## AUTHORS

## TITLE

Submitted (05-OCT-2001) Biologia Molecular, Hospital de la

Princesa, Diego de Leon 62, Madrid 28006, Spain

Sequence update by submitter

On Oct 5, 2001 this sequence version replaced gi:14278818.

## FEATURES

source

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/gene="DECTIN1"

gene

## CDS

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## ORIGIN

Alignment Scores: 3.92e-19 Length: 744  
 Pred. No.: 247.50 Matches: 50  
 Score: 247.50  
 Percent Similarity: 87.10% Conservative: 4  
 Best Local Similarity: 80.65% Mismatches: 3  
 Query Match: 53.57% Indels: 5  
 DB: 9 Gaps: 1

US-09-989-293A-377 (1-90) x AY026769 (1-744)

QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19  
 Db 157 CTATGCTTGGTAATACCTGGTGTCTGGTACCATGGCTATTGGAGATCC 216  
 QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39  
 Db 217 AATTCAAGGAAGCAACATCGAGATGGCTACTTTCTATCAAGAAATAAGAGAACCCAC 276  
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 Db 277 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAACC 336  
 QY 60 ThrGly 61  
 Db 337 ACAGGG 342

## RESULT 12

AF400601

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED



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QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 372 AATTTCAGGAAGCAACACATTGGAGTAATGGCTACTTCTTCAAGAAATTAAGAGAACCCAC 431
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 432 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGAGTGTCAAAACC 491
QY 60 ThrGly 61
Db 492 ACAGGG 497

RESULT 15
HSA312373
LOCUS HSA312373 1153 bp mRNA linear PRI 03-JUL-2001
DEFINITION Homo sapiens mRNA for DECTIN-1 receptor, splice variant 2.
ACCESSION AJ312373
VERSION AJ312373.1 GI:14599395
KEYWORDS alternative splicing; C-type lectin-1; DECTIN-1 gene; DECTIN-1 receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Sobanov,Y., Bernreiter,A., Derdak,S., Mechtcheriakova,D., Duechler,M., Kalthoff,F. and Hofer,E.
TITLE A novel cluster of lectin-like receptor genes expressed in monocytic, dendritic and endothelial cells maps close to the NK receptor genes in the human NK gene complex
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1153)
AUTHORS Sobanov,Y.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2001) Vascular Biology and Thrombosis Research, University of Vienna, Brunnerstrasse 59, Vienna A-1235, Austria
COMMENT Alternative splicing: See also AJ312372.
FEATURES
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/mol_type="mRNA"
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156..899
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NCVWIHVSIVYDQLCVSPSYSCIKKFSM"
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US-09-989-293A-377 (1-90) x HSA312373 (1-1153)
QY 5 LeuSerLeuLeuLeuLeuValCys-----GluAlaIleTpdArgSer 19
Db 312 CTATGCTTGGTAATACTGGTGATAGCTGTGCTCGGTACCATGGCTATTGGAGATCC 371
QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39
Db 372 AATTTCAGGAAGCAACACATTGGAGTAATGGCTACTTCTTCAAGAAATTAAGAGAACCCAC 431
QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59
Db 432 AGTCAACCCACACATCATCTTTAGAGACAGTGTGACTCTTACCAAGAGTGTCAAAACC 491
QY 60 ThrGly 61
Db 492 ACAGGG 497

Search completed: April 4, 2004, 09:09:38
Job time : 3398 secs
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Alignment Scores:

Pred. No.:	6,22e-19	Length:	1153
Score:	247.50	Matches:	50
Percent Similarity:	87.10%	Conservative:	4
Best Local Similarity:	80.65%	Mismatches:	3
Query Match:	53.57%	Indels:	5
DB:	9	Gaps:	1

ORIGIN

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 4, 2004, 07:56:38 ; Search time 2701 Seconds  
(without alignments)  
995.037 Million cell updates/sec

Title: US-09-989-293A-377  
Perfect score: 462  
Sequence: 1 MTFFLSLLLLVCEAIWRSN.....DSRGLILGAEWGRGVKKNT 90

Scoring table:  
Xgapop 10.0 , Xgapext 0.5  
Xgapop 10.0 , Xgapext 0.5  
Xgapop 6.0 , Xgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgm2\_1/USPTO.spool/US09989293/runat\_31032004\_081503\_14843/app\_query.fasta\_1.263  
-DB=EST -QFMT=fastcap -SUFFIX=rat -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09989293 @CGN 1\_1906 @runat\_31032004\_081503\_14843 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_htc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_htc.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rdm.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	365.5	79.1	663	9	AU185777	AU185777
C 2	306	66.2	800	14	CB958894	CB958894 AGENCOURT
C 3	247.5	53.6	659	12	BI018962	BI018962 IL3-MT026
C 4	209	45.2	663	28	AZ121459	AZ121459 RPCI-23-3
C 5	206	44.6	673	9	AV721179	AV721179 AV721179
C 6	174	37.7	582	14	CB420818	CB420818 593806 MA
C 7	138.5	30.0	855	12	BI107684	BI107684 602891529
C 8	82	17.7	833	10	BE865626	BE865626 601677978
C 9	82	17.7	924	12	BG165693	BG165693 602344512
C 10	81	17.5	1121	29	CNS04830	AL290421 Tetraodon
C 11	80.5	17.4	683	12	BI914658	BI914658 603179440
C 12	79	17.1	391	28	BH354332	BH354332 CH230-163
C 13	79	17.1	504	28	BH354326	BH354326 CH230-163
C 14	79	17.1	536	12	BJ193507	BJ193507 BJ193507
C 15	79	17.1	644	13	BQ406117	BQ406117 GA_Rd009
C 16	79	17.1	645	14	CF735257	CF735257 UT-W-HB0
C 17	78.5	17.0	884	29	CG183911	CG183911 PUC079TD
C 18	78.5	17.0	929	29	CG457562	CG457562 PUIKF73TD
C 19	78	16.9	649	29	CC701258	CC701258 OGWHR80TV
C 20	78	16.9	653	28	CC11703	CC11703 ii73e02.g
C 21	78	16.9	679	29	CG691911	CG691911 ZMMBBb028
C 22	78	16.9	723	29	AG009588	AG009588 Homo sapi
C 23	78	16.9	819	29	CC616498	CC616498 OGUFP08TH
C 24	77	16.7	477	12	BG276251	BG276251 uv02b11.y
C 25	77	16.7	626	28	AZ822524	AZ822524 2M095D21
C 26	77	16.7	943	13	BQ920084	BQ920084 AGENCOURT
C 27	77	16.7	967	28	B08136	B08136 F8C13-T7-1
C 28	77	16.7	1383	10	BF238075	BF238075 601811790
C 29	76.5	16.6	483	10	BE723365	BE723365 193059 MA
C 30	76.5	16.6	551	12	BI898668	BI898668 480374 MA
C 31	76.5	16.6	601	14	CB457947	CB457947 716067 MA
C 32	76.5	16.6	867	10	BF214995	BF214995 601847310
C 33	76	16.5	320	28	BH198757	BH198757 TC3-64015
C 34	76	16.5	781	13	BUS96994	BUS96994 AGENCOURT
C 35	76	16.5	968	28	BH135384	BH135384 ENTPA53TR
C 36	76	16.5	1007	29	CNS021MF	AL199104 Tetraodon
C 37	75.5	16.3	404	28	BH123205	BH123205 RPCI-24-2
C 38	75.5	16.3	504	8	AA614424	AA614424 nm89b06.s
C 39	75.5	16.3	774	12	BI553528	BI553528 603197519
C 40	75.5	16.3	879	13	BX346820	BX346820 BX346820
C 41	75.5	16.3	1006	13	BQ21671	BQ21671 AGENCOURT
C 42	75.5	16.3	1148	29	CG753752	CG753752 P048-4-H0
C 43	75	16.2	608	9	AV827009	AV827009 AV827009
C 44	75	16.2	672	29	CC615145	CC615145 OGVAG73TV
C 45	75	16.2	717	14	CF433331	CF433331 NIT1_26_G

# ALIGNMENTS

RESULT 1  
LOCUS AU185777/c  
DEFINITION AU185777 Homo sapiens Mast cell library (Sugita Y) Homo sapiens  
cdna clone B02302-019, mRNA sequence.  
ACCESSION AU185777  
VERSION AU185777.1 GI:14623690  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 663)

AUTHORS Sugita, Y., Oshida, T. and Oya, Y.  
 TITLE Human cDNA sequencing  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Yuji Sugita  
 Genex Research, Inc.  
 907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa 216-0001, Japan  
 Tel: 81-44-797-2281  
 Fax: 81-44-797-2622  
 Email: syuji@genex.co.jp, URL: http://www.genex.co.jp.

## FEATURES

source

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3052338"  
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 SfiI (ggcattatgcc); Site\_2: SfiI (ggcgccctcgcc);  
 Library is oligo-dr primed and directionally cloned. cDNA  
 was prepared from a glandular pool of tissues from thyroid,  
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
 adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGGCATATGCCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.38  
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 5.27e-36 Length: 663  
 Score: 365.50 Matches: 81  
 Percent Similarity: 89.01% Conservative: 0  
 Best Local Similarity: 89.01% Mismatches: 8  
 Query Match: 79.11% Indels: 3  
 DB: 9 Gaps: 1

US-09-989-293a-377 (1-90) x AU185777 (1-663)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTrp-ArgSerAs 20  
 Db 507 ATGACATTTTTCGGTCACNATTATNATGTTGGTATGTGAAGCTATTTGGNAGATCAA 448  
 Qy 20 nSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 40  
 Db 447 TTCAGNAGC---ACATTGNAAGATGGCTACTTTCTATCAAGAATAAAGAACACACAG 391  
 Qy 40 rGlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaValLysThrTh 60  
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 Qy 60 rGlyLysGlyLeuValLysGlyArgAsnLeuAspSerArgGlyLeuLeuGlyAlaGl 80  
 Db 331 AGGCAAGGGCAGTAGTTAAAGACGCAATCTTGACTCAAGAGGGTTAATCTTGTGTGTA 272  
 Qy 80 uAlaTrpGlyArgGlyValLysLysAsnThr 90  
 Db 271 AGCCTGGGCGAGGGGTGTAAAGAAAACACT 241

RESULT 2  
 CB958894 800 bp mRNA linear EST 29-APR-2003  
 LOCUS AGENCOURT 13785021 NIH MGC 184 Homo sapiens cDNA clone  
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 CB958894  
 ACCSSION CB958894.1 GI:30215010  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 800)  
 NIH-MGC http://www.ncbi.nlm.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

http://image.llnl.gov  
 Plate: NDCM151 row: e column: 19  
 High quality sequence stop: 488.

## FEATURES

source

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 /clone="IMAGE:3052338"  
 /lab\_host="DH10B (T1 phage-resistant)"  
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 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site\_1:  
 SfiI (ggcattatgcc); Site\_2: SfiI (ggcgccctcgcc);  
 Library is oligo-dr primed and directionally cloned. cDNA  
 was prepared from a glandular pool of tissues from thyroid,  
 parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
 adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CAGGCATATGCCC-3' and 3' adaptor sequence:  
 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.38  
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.69e-28 Length: 800  
 Score: 306.00 Matches: 70  
 Percent Similarity: 66.38% Conservative: 7  
 Best Local Similarity: 60.34% Mismatches: 10  
 Query Match: 66.23% Indels: 29  
 DB: 14 Gaps: 3

US-09-989-293a-377 (1-90) x CB958894 (1-800)

Qy 1 MetThrPheLeuSerLeuLeuLeuValCysGluAlaIleTrp-ArgSerAsn 20  
 Db 342 ATGACATTTTTCGTGCATATTATTATTCTGTGTATGTAAGCTATTTGGAGATCCAAT 401  
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 Db 402 TCAGGAGCACACATTCGAGAAATGGCTACTTCTTATCAAGAAATAAAGAACACACAGT 461  
 Qy 41 GlnProThrGlnSerLeuGluAspSerValThrProThrLysAlaVal-LysThrTh 60  
 Db 462 CAACCCACACATCACTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACACAC 521  
 Qy 60 rGly-----LysGlyLeuValLys-----GlyArgAsnLeuAspSerArgG1 74  
 Db 522 GGGGGTCTTTTCCAGCCCTTGTCTCCCAATTGGAATTATAATATGGAAGAAGAGC 581  
 Qy 74 yLeuIle-----  
 Db 582 TGTATTCTTTATCCAGCAATGTCCTAAATTTCCCTGGGGGATGGGAAGATAAAA 641  
 Qy 77 -----LeuGlyAlaGluAlaTrpGlyArgGlyValLys 87  
 Db 642 AAGACCAATGGGCTTGGGGCCAAACCTTGGGGCCCTTCCTAAAA 687

## RESULT 3

BI018962/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 659)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 AUTHORS

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

#### COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brasil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=IL3&t2=IL3-MT0267-050101-437-A02&t3=2001-01-05&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 639.

Location/Qualifiers

#### FEATURES

source

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/organism="Homo sapiens"

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/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="MT0267"

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SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

#### ORIGIN

Alignment Scores:

Pred. No.: 6,04e-21 Length: 659

Score: 247.50 Matches: 50

Percent Similarity: 87.10% Conservative: 4

Best Local Similarity: 80.65% Mismatches: 3

Query Match: 53.57% Indels: 5

DB: 12 Gaps: 1

US-09-989-293A-377 (1-90) x B1018962 (1-659)

QY 5 LeuSerLeuLeuLeuValCys-----GluAlaIleTrpArgSer 19

Db 617 CTATGCTTGGTAATCTGGTGAAGCTGTGGTCTGGTACATGGCTATTGGAGGTC 558

QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHis 39

Db 557 AATTCAAGGAGCAACACATGGAGATGGCTACTTCTCAAGAAATAAGAGAACAC 498

QY 40 SerGlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThr 59

Db 497 AGTCAACCCACACATCATCTTTTAGAGACAGTGTGACTCTCTACCAAAAGCTGTCAAACC 438

QY 60 ThrGly 61

Db 437 ACAGGG 432

RESULT 4

LOCUS AZ121459/c

DEFINITION RPCI-23-30A15-TV RPCI-23 Mus musculus genomic clone RPCI-23-30A15,

genomic survey sequence.

ACCESSION AZ121459

VERSION AZ121459.1 GI:7788387

#### KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

#### GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 663)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,

Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de

Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-30A15.TU

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page:

[http://www.tigr.org/tdb/bacends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bacends/mouse/bac_end_intro.html)

Plate: 30 row: A column: 15

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..663

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCI-23-30A15"

/sex="Female"

/lab\_host="DH10B"

/clone\_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:

EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methyase. Size

selected DNA was cloned into the pBACe3.6 vector at the

EcoRI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

#### ORIGIN

Alignment Scores:

Pred. No.: 5e-16 Length: 663

Score: 209.00 Matches: 50

Percent Similarity: 69.51% Conservative: 7

Best Local Similarity: 60.98% Mismatches: 22

Query Match: 45.24% Indels: 4

DB: 28 Gaps: 2

US-09-989-293A-377 (1-90) x AZ121459 (1-663)

QY 4 PheLeuSerLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySer 23

Db 248 TTTCTGTCTATCTATTGCTGTCTGTCGATGACGATATTTGTGTGACACATTCAGGGAGA 189

QY 24 AsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThr 43

Db 188 AATCCAGAGGAGAGAAACAACTTCTCTATCAAGAAATAAGAGAACACAC--AAGCCACA 132

QY 44 GlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrGlyGlyGly 63

Db 131 GAATCATCTTTAGATGAGAGAGTGGCTCCCTCCCAAGGCATCCCAACTTACGAGGAGGC 72

QY 64 IleValLysGlyA-gasn-----LeuAspSerArgGlyLeuIleLeuGlyAlaGluAla 81

Db 71 AGCAGAGAAAGAGGC--AATGGGATCCCGGATTCAGAGGTTTCATTTCTCTGGTCTGAGGCC 13



```

QY      82  Tipgly 83
      |||||
Db      12  TGGGT 7

RESULT 5
AV721179      AV721179      673 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION    AV721179 HTB Homo sapiens cDNA clone HTBAKFl1 5', mRNA sequence.
ACCESSION     AV721179
VERSION       AV721179.1 GI:10818331
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 673)
AUTHORS       Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
              Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
              Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
              Chen,J., Chen,Z. and Han,Z.
TITLE         Homo sapiens cDNA HTB clones
JOURNAL       Unpublished (2000)
COMMENT       Contact: Zeguang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex. 45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.

FEATURES      Location/Qualifiers
              source          1..673
              mol_type="mRNA"
              db_xref="taxon:9606"
              clone="HTBAKFl1"
              tissue type="Hypothalamus"
              dev stage="Adult"
              lab_host="SOLR"
              clone_lib="HTB"
              note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
              XhoI"

ORIGIN
Alignment Scores:
Pred. No.:      1,23e-15      Length:      673
Score:          206.00      Matches:      40
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     44.59%      Indels:      0
DB:              9      Gaps:        0

US-09-989-293A-377 (1-90) x AV721179 (1-673)

QY      22  GlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGln 41
      |||||
Db      2  GGAAGCAACATTCGAGATGGCTTCTTATCAAGAAATAAGAGACACACAGTCAA 61
      |||||
QY      42  ProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      62  CCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACAGGG 121
      |||||

RESULT 6
CB420818
LOCUS        CB420818      582 bp      mRNA      linear      EST 25-MAR-2003
DEFINITION    593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION     CB420818
VERSION       CB420818.1 GI:29187264
KEYWORDS      EST.
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

QY      5  LeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn 24
      |||||
Db      214  CTGGTGATGAATCTGTGGTCCTGAGTACCTCGGGTATTTGGAGATCCAGTTTCAGGGAACAAC 273
      |||||
QY      25  ThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGln 44
      |||||
Db      274  CTGTTGAAGAGTGACAGCTTTCCATCATCAAGAAATAAGACACACACAGACTCAACCCACAAA 333
      |||||
QY      45  SerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      334  TCATCTTTAGAGATAGTGTGATACCTACCAAGGCTCTCACGACCACAGGA 384
      |||||

RESULT 7
B1107684
LOCUS        B1107684      855 bp      mRNA      linear      EST 26-JUN-2001
DEFINITION    602891529F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036647 5',
              mRNA sequence.
ACCESSION     B1107684
VERSION       B1107684.1 GI:14558577
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 855)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
JOURNAL       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.

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QY      82  Tipgly 83
      |||||
Db      12  TGGGT 7

RESULT 5
AV721179      AV721179      673 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION    AV721179 HTB Homo sapiens cDNA clone HTBAKFl1 5', mRNA sequence.
ACCESSION     AV721179
VERSION       AV721179.1 GI:10818331
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 673)
AUTHORS       Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
              Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
              Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
              Chen,J., Chen,Z. and Han,Z.
TITLE         Homo sapiens cDNA HTB clones
JOURNAL       Unpublished (2000)
COMMENT       Contact: Zeguang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919(ex. 45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.

FEATURES      Location/Qualifiers
              source          1..673
              mol_type="mRNA"
              db_xref="taxon:9606"
              clone="HTBAKFl1"
              tissue type="Hypothalamus"
              dev stage="Adult"
              lab_host="SOLR"
              clone_lib="HTB"
              note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
              XhoI"

ORIGIN
Alignment Scores:
Pred. No.:      1,23e-15      Length:      673
Score:          206.00      Matches:      40
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     44.59%      Indels:      0
DB:              9      Gaps:        0

US-09-989-293A-377 (1-90) x AV721179 (1-673)

QY      22  GlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGln 41
      |||||
Db      2  GGAAGCAACATTCGAGATGGCTTCTTATCAAGAAATAAGAGACACACAGTCAA 61
      |||||
QY      42  ProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      62  CCCACACATCATCTTTAGAGACAGTGTGACTCTCTACCAAGCTGTCAAAACCCACAGGG 121
      |||||

RESULT 6
CB420818
LOCUS        CB420818      582 bp      mRNA      linear      EST 25-MAR-2003
DEFINITION    593806 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION     CB420818
VERSION       CB420818.1 GI:29187264
KEYWORDS      EST.
SOURCE        Bos taurus (cow)
ORGANISM      Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

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REFERENCE     1 (bases 1 to 582)
AUTHORS       Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
              Wray,J.B. and Keele,J.W.
TITLE         A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL       Unpublished (2003)
COMMENT       Contact: Smith TPL
              USDA, ARS, US Meat Animal Research Center
              PO Box 166, Clay Center, NE 68933-0166, USA
              Tel: 402 762 4366
              Fax: 402 762 4390
              Email: smith@email.marc.usda.gov
              Single pass sequencing. Bases called with phred v0.020425.c and
              trimmed with the aid of the trim_alt option. Vector identified with
              cross match v0.990329.
              Plate: FQY8014 row: B column: 7
              Seq primer: GTAATFACGACTCATTATAGG.
              Location/Qualifiers
              source          1..582
              organism="Bos taurus"
              mol_type="mRNA"
              db_xref="taxon:9913"
              tissue type="pooled"
              lab_host="DH10B"
              clone_lib="MARC 6BOV"
              notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
              Library made with RNA pooled from multiple tissues
              including liver, lung, hypothalamus, pituitary, and
              placenta/endometrium."

ORIGIN
Alignment Scores:
Pred. No.:      1,23e-11      Length:      582
Score:          174.00      Matches:      35
Percent Similarity: 77.19%      Conservative: 9
Best Local Similarity: 61.40%      Mismatches: 13
Query Match:     37.66%      Indels:      0
DB:              14      Gaps:        0

US-09-989-293A-377 (1-90) x CB420818 (1-582)

QY      5  LeuSerLeuLeuLeuLeuValCysGluAlaIleTrpArgSerAsnSerGlySerAsn 24
      |||||
Db      214  CTGGTGATGAATCTGTGGTCCTGAGTACCTCGGGTATTTGGAGATCCAGTTTCAGGGAACAAC 273
      |||||
QY      25  ThrLeuGluAsnGlyTyrPheLeuSerArgAsnLysGluAsnHisSerGlnProThrGln 44
      |||||
Db      274  CTGTTGAAGAGTGACAGCTTTCCATCATCAAGAAATAAGACACACACAGACTCAACCCACAAA 333
      |||||
QY      45  SerSerLeuGluAspSerValThrProThrLysAlaValLysThrThrGly 61
      |||||
Db      334  TCATCTTTAGAGATAGTGTGATACCTACCAAGGCTCTCACGACCACAGGA 384
      |||||

RESULT 7
B1107684
LOCUS        B1107684      855 bp      mRNA      linear      EST 26-JUN-2001
DEFINITION    602891529F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5036647 5',
              mRNA sequence.
ACCESSION     B1107684
VERSION       B1107684.1 GI:14558577
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 855)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
JOURNAL       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Gilbert Smith, Ph.D.
              cDNA Library Preparation: Life Technologies, Inc.

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source      1. 924
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4454450"
            /tissue_type="hypernephroma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_89"
            /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
            Average insert size 1.3 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 12.9      Length: 924
Score: 82.00        Matches: 30
Percent Similarity: 40.00%      Conservative: 14
Best Local Similarity: 27.27%   Mismatches: 22
Query Match: 17.75%            Indels: 44
DB: 12                  Gaps: 5

US-09-989-293A-377 (1-90) x BG165693 (1-924)
QY      4 PheLeuSerLeuLeuLeuVal-----CysGluAlaIle 16
Db      534 TTCTCAGCTCTTCCTCTCTGTCATCTGCTCCACCATGCTCATTTGCTTCAGTATC 475

QY      17 TrpArgSerAsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSerArgAsnLys 36
Db      474 CTCACATTCATTTCTTCATCAGATCAATA----- 445

QY      37 GluAsnHisGlnProThrGlnSerSerLeuGluAspSerVal----- 51
Db      444 TCTTCCCAATCGTCTCCATCCAGCTCCTCTCTCCCTCCCTGCTGCTCTCTCTCTGCTGC 385

QY      52 -----ThrProThrAlaValLysThrThrGlyLysGlyIleValLysGlyArgAsn 69
Db      384 TTTCACCTCTTCGCTGCTGTTCACACCACTGAGCGGGGGT----- 337

QY      70 LeuAspSerArgGlyLeuLeuLeuGlyAlaGluAla----- 81
Db      336 ---TCTCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280

QY      82 -----TyrGlyArg 84
Db      279 CTGCGCTCTTTCAGCGCTGGGGGCGC 250

RESULT 10
CNS04H30      1121 bp      DNA      linear      GSS 01-SEP-2000
LOCUS      Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION  109N19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION  AL290421
VERSION    AL290421.1 GI:8029001
KEYWORDS  GSS: genome survey sequence.
SOURCE    Tetraodon nigroviridis
ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizanes,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE        Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
JOURNAL      Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE     20296633
PUBMED      10835645

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REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizanes,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
TITLE        Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE     20359837
PUBMED      10899143
SOURCE      3 (bases 1 to 1121)
            Genoscope.
REFERENCE    Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT      This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES
            Location/Qualifiers
            source          1..1121
                           /organism="Tetraodon nigroviridis"
                           /mol_type="genomic DNA"
                           /db_xref="taxon:99883"
                           /clone="109N19"
                           /clone_lib="G"
                           /note="Genoscope sequence ID : COBG109CG101P1-end : T7"

ORIGIN
Alignment Scores:
Pred. No.: 22.7      Length: 1121
Score: 81.00        Matches: 33
Percent Similarity: 38.10%      Conservative: 7
Best Local Similarity: 31.43%   Mismatches: 37
Query Match: 17.53%            Indels: 28
DB: 29                Gaps: 4

US-09-989-293A-377 (1-90) x CNS04H30 (1-1121)
QY      2 ThrPhePheLeuSerLeuLeuLeuValCys-----GluAlaIleTyr 17
Db      739 ACACACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 798

QY      18 ArgSerAsn-----SerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSer 33
Db      799 AAACATCTCGAACCCGACCTTACCAACAGCAAACTGATGAAACCGTTTGTCTCTCA 858

QY      34 ArgAsnLysGluAsn----- 38
Db      859 TAAACGCTGTGAGAACTGATAGTAAAGGGAGCCAGCGCTTCAGCTTACCTGCTCAGGTGT 918

QY      39 -----HisSerGlnProThrGlnSerSerLeuGluAspSerVal-----Pro 53
Db      919 TCAGTCCACAGTCTCTCTCCAGCTATGACACTTTTACTTTCTCTCTCTCTCTCTCTCTCT 978

QY      54 ThrLysAlaValLysThrThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg 73
Db      979 ACCAGTTTTTGTGCTGCTGCGCGGGAAGTAGGATAATCTCTGCGCGGAATCTTGCTCTGAA 1038

QY      74 GlyLeuLeuLeuGly 78
Db      1039 AACTTTGACCTCGGG 1053

RESULT 11
BI914658/c
LOCUS      BI914658      683 bp      mRNA      linear      EST 17-OCT-2001
DEFINITION 603179440F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243769 5',
            mRNA sequence.
ACCESSION  BI914658
VERSION    BI914658.1 GI:16199003
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 683)

## AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [rcapbs@mail.nih.gov](mailto:rcapbs@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM11614 row: p column: 10  
High quality sequence stop: 668.

## FEATURES

source

1..683  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5243769"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_121"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Pred. No.: 13.2 Length: 683  
Score: 80.50 Matches: 25  
Percent Similarity: 54.72% Conservative: 4  
Best Local Similarity: 47.17% Mismatches: 15  
Query Match: 17.42% Indels: 9  
DB: 12 Gaps: 5

US-09-989-293A-377 (1-90) x B1914658 (1-683)

QY 39 HisSerGlnProThrGlnSer-----SerLeuGluAspSerValThrProThr 54  
Db 515 CACCAGCGCAATGCAAGCTCGGGGCATCAAGGCTCAGTGTCTGGGACAGTCTGCTACCTAGC 456  
QY 55 LysAlaValLysThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg--- 73  
Db 455 TCTGCTTC--TGTACACAGCTCTGTCATAGTTGGGGGTACACATAGATAGGAG 399  
QY 74 GlyLeuIleLeuGlyAlaGluAlaTrp---GlyArgGly 85  
Db 398 GGC-----CTGGGTTTCAGGGGCTGGCAGGCGCAGGGG 366

RESULT 12  
BH354332/c  
LOCUS BH354332/c 391 bp DNA linear GSS 03-DEC-2001  
DEFINITION CH230-163F16.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone  
CH230-163F16, genomic survey sequence.

## ACCESSION

BH354332

## VERSION

BH354332.1 GI:17285066

## KEYWORDS

GSS.

## SOURCE

Rattus norvegicus (Norway rat)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 391)

## AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Teegave, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.

## TITLE

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

## JOURNAL

Unpublished (1999)

## COMMENT

Other GSSs: CH230-163F16.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [szhao@tigr.org](mailto:szhao@tigr.org)  
Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@email.cho.org](mailto:pdejong@email.cho.org)). Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/orering\\_information.htm](http://www.chori.org/bacpac/orering_information.htm)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
Plate: 163 row: F column: 16  
Seq primer: SP6  
Class: BAC ends.

## FEATURES

source

1..391  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SHSd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-163F16"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 1"  
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CHORI-230 Rat (BN/SHSd/MCW) BAC library produced by Pieter de Jong"

## ORIGIN

## Alignment Scores:

Pred. No.: 9.46 Length: 391  
Score: 79.00 Matches: 22  
Percent Similarity: 46.38% Conservative: 10  
Best Local Similarity: 31.88% Mismatches: 23  
Query Match: 17.10% Indels: 14  
DB: 28 Gaps: 1

US-09-989-293A-377 (1-90) x BH354332 (1-391)

QY 34 ArgAsnLysGluAsnHisSerGlnProThrGlnSerSerLeuGluAspSerValThrPro 53  
Db 334 AGGGGTTCCCTGTAATTTCTCTTCACATCTCAGTCCTCATGCTCTGCAATATCACTATT 275  
QY 54 ThrLysAlaValLysThrGlyLysGlyIleValLysGlyArgAsnLeuAspSerArg 73  
Db 274 TCTAAGTTAAACAAAGTCCGGGTCGTGGGTACTGATGATGACACAGAGGAATCTAAC 215  
QY 74 Gly-----LeuIleLeuGlyAla 79  
Db 214 GGGAGAACTAATGCTTCCAACACAGACCATCAGTGGAAACTGCTTATGTGACGGCAA 155  
QY 80 GluAlaTrpGlyArgGlyValLys 88  
Db 154 GAGGTGTTTGAAGAGGGGGGGAAG 128

## RESULT 13

BH354326/c

## LOCUS

BH354326/c

## DEFINITION

CH230-163F15.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone

## ACCESSION

BH354326

## VERSION

BH354326.1 GI:17285060

## KEYWORDS

GSS.

## SOURCE

Rattus norvegicus (Norway rat)

## ORGANISM

Rattus norvegicus



QY 41 GlnProThrGlnSerSerLeuGluAspSerValThrProThrLysAlaValLysThrThr 60  
 Db 295 CCAACACACCTCCGACATCGTGTGATGATGATCCTCGACACTCCTCTTCTCGCAAGCTT 236  
 QY 61 GlyLysGlyIleValLysGlyArg-----AsnLeuAspSerArgGlyLeuIle 76  
 Db 235 GCGGAA-----CAGGAGGCGCAGTATCCTCACTGAGACATTCGGCGCTTAAC 185  
 QY 77 LeuGlyAlaGluAlaTrpGlyArg 84  
 Db 184 CAAAGCAGCGATCTTCTCGCGCGT 161

## RESULT 15

BQ406117 644 bp mRNA linear EST 22-MAY-2002  
 GA\_Ed0090H12f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arboreum cDNA clone GA\_Ed0090H12f, mRNA sequence.

ACCESSION BQ406117

VERSION BQ406117.1

KEYWORDS GI:21093804

SOURCE EST.

ORGANISM Gossypium arboreum

Gossypium arboreum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1. (bases 1 to 644)

Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,

Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

An integrated analysis of the genetics, development, and evolution

of the cotton fiber

Unpublished (2000)

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total High Quality bases = 584

Seq primer: TAATACGACTCACTATAGG

High quality sequence stop: 629.

FEATURES

Location/Qualifiers

1..644

/organism="Gossypium arboreum"

/mol\_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db\_xref="taxon:29729"

/clone="GA\_Ed0090H12f"

/tissue\_type="Fibers isolated from bolls harvested 7-10

dpa"

/lab\_host="E. coli"

/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"

/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Alignment Scores:

Pred. No.: 18.9 Length: 644

Score: 79.00 Matches: 25

Percent Similarity: 46.15% Conservative: 11

Best Local Similarity: 32.05% Mismatches: 24

Query Match: 17.10% Indels: 18

DB: 13 Gaps: 3

US-09-989-293A-377 (1-90) x BQ406117 (1-644)

QY 20 AsnSerGlySerAsnThrLeuGluAsnGlyTyrPheLeuSer-----ArgAsnLysGlu 37

Db 310 CACTCACCAACACCAACAGCTGCAGATGGGTTCTTCTTCAAGACACCGTATAGCAA 369

QY 38 AsnHisSerGlnProThrGlnSerSerLeuGluAspSerVal----- 51

Db 370 CAGCAGGCACTGCCTTCAGGATCATCAACTTCAACGTCAGTGTGTCATTGTTCTCCA 429  
 QY 52 -----ThrpThrLysAlaValLysThrThrGlyLys 62  
 Db 430 GTTACTCCTGTAACTACTGGCACCACTGACCCCTGCAAGGCTGTA---GTTGCTGCTGCT 486  
 QY 63 GlyIleValLysGlyValArgAsnLeuAspSerArgGlyLeuIleLeuGlyAlaGlu 80  
 Db 487 GGTAAATATGAAGAGTGTGGCATAGCATCACAGGCACTTATACATGCTGCACAA 540

Search completed: April 4, 2004, 09:54:24  
 Job time : 2717 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2004, 12:07:55 ; Search time 14 Seconds  
(without alignments)  
334.737 Million cell updates/sec

Title: US-09-989-293A-377

Perfect score: 462

Sequence: 1 MFFFLSLLLLVCEAIWRN.....DSRGLILGAENGWGKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68.5	14.8	622	TFRL_RAT	Q99376 rattus norv
2	67	14.5	226	RS5_MYCGA	O52349 mycoplasma
3	65	14.1	368	VE2_HPV52	P36796 human papil
4	64	13.9	255	RR3_CHAGL	Q8m9v0 chaetosphe
5	63.5	13.7	669	GALC_HUMAN	P54803 homo sapien
6	63.5	13.7	705	CDGS_YEAST	P32582 saccharomyc
7	63.5	13.7	882	KEL2_YEAST	P50090 saccharomyc
8	63	13.6	80	DMS6_AGAAN	Q93226 agalychnais
9	62.5	13.5	268	PYRF_PACTA	Q93864 pachysolen
10	62.5	13.5	379	Y528_SUNY3	Q55518 synchocyst
11	62	13.4	1634	DPOL_METJA	Q58295 methanococc
12	61.5	13.3	401	TRML_AERPE	Q9ydv7 aeropyrum p
13	61.5	13.3	516	MEFA_XENLA	Q03414 xenopus lae
14	61.5	13.3	834	CWFM_SCHPO	Q9p6r5 schizosacch
15	61.5	13.3	960	YMX6_YEAST	Q04279 saccharomyc
16	61	13.2	237	T4S3_HUMAN	P19075 homo sapien
17	61	13.2	415	B2AR_MACMU	Q28509 macaca mula
18	61	13.2	790	LY14_YEAST	P40971 saccharomyc
19	61	13.2	1774	MSAS_PENPA	P22367 penicillium
20	60.5	13.1	567	TGR2_RAT	P38438 rattus norv
21	60.5	13.1	676	RLM1_YEAST	Q12224 saccharomyc
22	60.5	13.1	708	ICAL_HUMAN	P20810 homo sapien
23	60.5	13.1	1369	NFAS_CHICK	O42414 gallus gall
24	60.5	13.1	1969	2292_HUMAN	O60281 homo sapien
25	60.5	13.1	2298	CU05_HUMAN	Q9y3r5 homo sapien
26	60	13.0	653	RAE1_HUMAN	P24386 homo sapien
27	60	13.0	671	NCPR_MUSDO	Q07994 musca domes
28	60	13.0	938	SVI_BUCBP	Q8k922 buchnera ap
29	60	13.0	939	SVI_BUCBP	Q89au9 buchnera ap
30	60	13.0	962	SUTR_DROME	Q9vts2 drosophila
31	60	13.0	1503	KRP6_HUMAN	Q95255 homo sapien
32	59.5	12.9	576	UN87_CABEL	P37806 caenorhabdi
33	59	12.8	202	RUVA_PSESM	Q87y34 pseudomonas

34	59	12.8	641	UGS2_SOLTU	P93568 solanum tub
35	59	12.8	708	MM09_RAT	P50282 rattus norv
36	59	12.8	719	CLID_BACTU	Q9xdl1 bacillus th
37	59	12.8	793	YF06_MYCPN	P75280 mycoplasma
38	59	12.8	970	DAB1_YEAST	P21657 saccharomyc
39	59	12.8	1116	MRH1_SCHPO	Q10407 schizosacch
40	58.5	12.7	417	OXLT_OXAFO	Q51330 oxalobacter
41	58.5	12.7	439	QUIX_ACICA	Q43923 acinetobact
42	58.5	12.7	531	SIS2_CANTR	Q12600 candida tro
43	58.5	12.7	542	THS_METJA	Q58405 methanococc
44	58.5	12.7	953	LKA1_PASHA	P16535 pasteurella
45	58.5	12.7	953	LKA3_PASHA	P55116 pasteurella

## ALIGNMENTS

### RESULT 1

ID	TFRL_RAT	STANDARD;	PRT;	622 AA.
AC	Q99376;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Transferrin receptor protein 1 (TfR1) (TfR) (TfR) (Fragment).			
GN	TFRC OR TRFR.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=91125359; PubMed=2126342;			
RA	Roberts K.P., Griswold M.D.;			
RT	"Characterization of rat transferrin receptor cDNA: the regulation of			
RT	transferrin receptor mRNA in testes and in Sertoli cells in culture."			
RL	Mol. Endocrinol. 4:531-542(1990).			
CC	-I- FUNCTION: Cellular uptake of iron occurs via receptor-mediated			
CC	endocytosis of ligand-occupied transferrin receptor into			
CC	specialized endosomes. Endosomal acidification leads to iron			
CC	release. The apotransferrin-receptor complex is then recycled to			
CC	the cell surface with a return to neutral pH and the concomitant			
CC	loss of affinity of apotransferrin for its receptor. Transferrin			
CC	receptor is necessary for development of erythrocytes and the			
CC	nervous system (By similarity).			
CC	-I- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin			
CC	molecule per polypeptide chain (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).			
CC	-I- TISSUE SPECIFICITY: In testis, expressed in Sertoli cells,			
CC	peritubular myoid cells and in germinal cells. Highest levels in			
CC	Sertoli cells.			
CC	-I- PTM: N- and O-glycosylated, phosphorylated and palmitoylated (By			
CC	similarity).			
CC	-I- SIMILARITY: Belongs to peptidase family M28B.			

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EMBL; M58040; AAA42273.1; --  
PIR; A34549; A34549.  
HSSP; P02786; 1CX8.  
InterPro; IPR003137; PA.  
InterPro; IPR007484; Peptidase\_M28.  
InterPro; IPR007365; TFR\_dimer.  
Pfam; PF02225; PA; 1.  
Pfam; PF04389; Peptidase\_M28; 1.  
Pfam; PF04253; TFR\_dimer; 1.





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CC EMBL; X74481; CAA52588.1; -.
DR DR
DR PIR; S36576; S36576.
DR HSP; P17383; 1DHM.
DR InterPro; IPR000427; E2.C.
DR InterPro; IPR001866; E2.N.
DR InterPro; IPR009021; Viral_DNA_bd.
DR Pfam; PF00511; E2.C; 1.
DR Pfam; PF00508; E2.N; 1.
DR ProDom; PD000672; E2.C; 1.
DR ProDom; PD000678; E2.N; 1.
DR Early protein; Transcription regulation; Activator; DNA-binding;
KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
SQ SEQUENCE 368 AA; 4739 MW; 3212B423B2F629D3 CRC64;

Query Match 14.1%; Score 65; DB 1; Length 368;
Best Local Similarity 27.0%; Pred. No. 15;
Matches 24; Conservative 11; Mismatches 40; Indels 14; Gaps 3;

QY 10 LLVCEAIWNSGNSNTLENGYFLSRN-----KENHSQPTQSSLEDSVTPTKAVK 58
DB 192 VIVCPASVSNSEVSTT-ETAVHLCTETSKTSVSVGAKDTHLPQPKRRRPDVTDSRNTK 250
QY 59 TTGKGIVKGRNLD--RGLILGAEAWGRG 85
DB 251 YFNILLRQQSVDSYTRGLVTATCTCNKG 279

RESULT 4
RR3 CHAGL STANDARD; PRT; 255 AA.
AC QM3Y0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S3.
GN RPS3.
OS Chaetosphaeeridium globosum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Coleochaetales;
OC Chaetosphaeeridiaceae; Chaetosphaeeridium.
OC NCBI_TaxID=96477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1311;
RX MEDLINE=22177139; PubMed=12161560;
RA Turmel M., Otis C., Lemieux C.;
RT "The chloroplast and mitochondrial genome sequences of the charophyte
RT Chaetosphaeeridium globosum: insights into the timing of the events
RT that restructured organelle DNAs within the green algal lineage that
RT led to land plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:11275-11280(2002).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the S3p family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; AF94278; AAM06576.1; -.
DR HAMAP; MF_01309; -.
DR InterPro; IPR009019; KH_prok.
DR InterPro; IPR004044; KH_TYPE_2.
DR InterPro; IPR001351; Ribosomal_S3_C.
DR InterPro; IPR008282; Ribosomal_S3_N.
DR Pfam; IPR005704; S3_bact.
DR Pfam; PF00189; Ribosomal_S3_C; 1.
```

```
DR Pfam; PF00417; Ribosomal_S3_N; 1.
DR TIGRFam; TIGR01009; rpsC_bact; 1.
DR PROSITE; PS00823; KH_TYPE_2; FALSE_NEG.
DR PROSITE; PS00548; RIBOSOMAL_S3; 1.
KW Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
FT DOMAIN 51 124 KH TYPE-2.
SQ SEQUENCE 255 AA; 29494 MW; 0A88CEB18062EAC1 CRC64;

Query Match 13.9%; Score 64; DB 1; Length 255;
Best Local Similarity 30.3%; Pred. No. 13;
Matches 27; Conservative 9; Mismatches 35; Indels 18; Gaps 4;

QY 14 EAIMSNSGNSNTLENGYF---LSRNKENHSQPT-----QSSLEDSVTPTKAVTKG-- 62
DB 127 EKWRYVQESLTLNSGKFRMTLSKYSNPYKEANIVAEYIARQLENRVAFRRAMKQAKDA 186
QY 63 ----GIVKGRNLDRLGLIGAE-----AWGR 84
DB 187 KENGQVKGIKIQISGLNGAETARVEWAR 215

RESULT 5
GALC_HUMAN STANDARD; PRT; 669 AA.
AC P54803;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Galactocerebrosidase precursor (EC 3.2.1.46) (GALCERase)
DE (Galactosylceramide) (Galactosylceramide beta-galactosidase)
DE (Galactocerebroside beta-galactosidase).
GN GALC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.
RC TISSUE=Placenta, and Skin fibroblast;
RX MEDLINE=94128088; PubMed=8297359;
RA Sakai N., Inui K., Fujii N., Fukushima H., Nishimoto J.,
RA Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
RT "Krabbe disease: isolation and characterization of a full-length cDNA
RT for human galactocerebrosidase.";
RL Biochem. Biophys. Res. Commun. 198:485-491(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 27-59 AND 436-454.
RC TISSUE=Brain, and Testis;
RX MEDLINE=94108435; PubMed=8281145;
RA Chen Y.Q., Rafi M.A., de Gala G., Wenger D.A.;
RT "Cloning and expression of cDNA encoding human galactocerebrosidase,
RT the enzyme deficient in globoid cell leukodystrophy.";
RL Hum. Mol. Genet. 2:1841-1845(1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT THR-546.
RX MEDLINE=95324938; PubMed=7601472;
RA Luzi P., Rafi M.A., Wenger D.A.;
RT "Structure and organization of the human galactocerebrosidase (GALC)
RT gene.";
RL Genomics 26:407-409(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98094242; PubMed=9434153;
RA Sakai N., Fukushima H., Inui K., Fu L., Nishigaki T., Yanagihara I.,
RA Tatsumi N., Ozono K., Okada S.;
RT "Human galactocerebrosidase gene: promoter analysis of the 5'-flanking
RT region and structural organization.";
RL Biochim. Biophys. Acta 1395:62-67(1998).
RN [5]
RP SEQUENCE OF 27-45 AND 436-454, AND CHARACTERIZATION.
RC TISSUE=Urine;
RX MEDLINE=94002192; PubMed=8399327;
RA Chen Y.Q., Wenger D.A.;
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RT "Galactocerebrosidase from human urine: purification and partial  
RT characterization.";  
RL Biochim. Biophys. Acta 1170:53-61(1993).  
RN [6]  
RP REVIEW ON GLD MUTATIONS.  
RX MEDLINE=97478285; PubMed=9338580;  
RA Wenger D.A., Rafi M.A., Luzzi P.;  
RT "Molecular genetics of Krabbe disease (globoid cell leukodystrophy):  
RT diagnostic and clinical implications.";  
RL Hum. Mutat. 10:268-279(1997).  
RN [7]  
RP REVIEW ON VARIANTS.  
RX MEDLINE=20295342; PubMed=10833326;  
RA Wenger D.A., Rafi M.A., Luzzi P., Datto J., Costantino-Cecarini E.;  
RT "Krabbe disease: genetic aspects and progress toward therapy.";  
RL Mol. Genet. Metab. 70:1-9(2000).  
RN [8]  
RP VARIANT CYS-168.  
RX MEDLINE=96090246; PubMed=7581365;  
RA Rafi M.A., Luzzi P., Chen Y.Q., Wenger D.A.;  
RT "A large deletion together with a point mutation in the GALC gene is a  
RT common mutant allele in patients with infantile Krabbe disease.";  
RL Hum. Mol. Genet. 4:1285-1289(1995).  
RN [9]  
RP VARIANTS GLD ALA-302 AND GLY-550.  
RX MEDLINE=96121583; PubMed=8595408;  
RA Tatsumi N., Inui K., Sakai N., Fukushima H., Nishimoto J.,  
RA Yanagihara I., Nishigaki T., Tsukamoto H., Fu L., Tanikie M.,  
RA Okada S.;  
RT "Molecular defects in Krabbe disease.";  
RL Hum. Mol. Genet. 4:1865-1868(1995).  
RN [10]  
RP VARIANTS GLD HIS-63; SER-95; LEU-101; THR-234; SER-268 AND CYS-298,  
RP AND VARIANT THR-546.  
RX MEDLINE=97094180; PubMed=8940268;  
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,  
RA MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.;  
RT "Molecular heterogeneity of late-onset forms of globoid-cell  
RT leukodystrophy.";  
RL Am. J. Hum. Genet. 59:1233-1242(1996).  
RN [11]  
RP ERRATUM.  
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,  
RA MacFarlane H., Gusella J.F., Krivit W., Kolodny E.H.;  
RL Am. J. Hum. Genet. 60:1264-1264(1997).  
RN [12]  
RP VARIANTS GLD ASN-528 AND SER-583.  
RX MEDLINE=96198195; PubMed=8786069;  
RA Rafi M.A., Luzzi P., Zlotogora J., Wenger D.A.;  
RT "Two different mutations are responsible for Krabbe disease in the  
RT Druze and Moslem Arab populations in Israel.";  
RL Hum. Genet. 97:304-308(1996).  
RN [13]  
RP VARIANTS GLD MET-66; ASP-270 AND SER-618, AND VARIANTS VAL-289 AND  
RP THR-546.  
RX MEDLINE=97418134; PubMed=9272171;  
RA Fukuya H., Kukita Y.-J., Nagano S., Sakai Y., Yamashita Y.,  
RA Fuyukawa H., Inatomi Y., Saito Y., Koike R., Tsuji S., Fukumaki Y.,  
RA Hayashi K., Kobayashi T.;  
RT "Adult onset globoid cell leukodystrophy (Krabbe disease): analysis of  
RT galactosylceramidase cDNA from four Japanese patients.";  
RL Hum. Genet. 100:450-456(1997).  
RN [14]  
RP VARIANTS GLD ASP-270 AND ARG-537, AND VARIANT THR-625.  
RX MEDLINE=99406501; PubMed=10477434;  
RA De Gasperi R., Gama Sosa M.A., Sartorato E.L., Battistini S.,  
RA Raghavan S., Kolodny E.H.;  
RT "Molecular basis of late-life globoid cell leukodystrophy.";  
RL Hum. Mutat. 14:256-262(1999).  
RN [15]  
RP VARIANTS GLD ARG-43; PHE-52; ILE-262; CYS-319; GLY-410; HIS-515 AND  
RP ARG-652.  
RX MEDLINE=99250870; PubMed=10234611;

RA Fu L., Inui K., Nishigaki T., Tatsumi N., Tsukamoto H., Kokubu C.,  
RA Muramatsu T., Okada S.;  
RT "Molecular heterogeneity of Krabbe disease.";  
RL J. Inher. Metab. Dis. 22:155-162(1999).  
RN [16]  
RP FUNCTION: Hydrolyzes the galactose ester bonds of  
CC galactosylceramide, galactosylsphingosine, lactosylceramide, and  
CC monogalactosylglyceride. Enzyme with very low activity  
CC responsible for the lysosomal catabolism of galactosylceramide, a  
CC major lipid in myelin, kidney and epithelial cells of small  
CC intestine and colon.  
CC CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)O = D-  
CC galactose + N-acylsphingosine.  
CC SUBCELLULAR LOCATION: Lysosomal.  
CC ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P54803-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=P54803-2; Sequence=VSP\_001800, VSP\_001801;  
CC TISSUE SPECIFICITY: Highest level of activity in testes compared  
CC to brain, kidney, placenta and liver. Can also be found in urine.  
CC POLYMORPHISM: Polymorphic amino-acid changes are responsible for  
CC the wide range of catalytic activities found in the general  
CC population.  
CC DISEASE: Defects in GALC are the cause of globoid cell  
CC leukodystrophy (GLD) [MIM:245200]; also known as Krabbe disease.  
CC This autosomal recessive disorder results in the insufficient  
CC catabolism of several galactolipids that are important in the  
CC production of normal myelin. Clinically, the most frequent form is  
CC the infantile form. Most patients (90%) present before six months  
CC of age with irritability, spasticity, arrest of motor and mental  
CC development, and bouts of temperature elevation without infection.  
CC This is followed by myoclonic jerks of arms and legs,  
CC opisthotonus, hypertonic fits, and mental regression, which  
CC progresses to a severe decerebrate condition with no voluntary  
CC hyperreflexia before 2 years of age. However, a significant number  
CC of cases with later onset, presenting with unexplained blindness,  
CC weakness and/or progressive motor, and sensory neuropathy that can  
CC progress to severe mental incapacity and death, have been  
CC identified.  
CC MISCELLANEOUS: Has an optimal pH between 4.0 and 4.4. Activity is  
CC lost when heated at 52 degrees Celsius for five minutes.  
CC SIMILARITY: Belongs to family 59 of glycosyl hydrolases.  
CC DATABASE: NAME=GeneDis; NOTE=Krabbe disease;  
CC WWW=http://life2.tau.ac.il/GeneDis/Tables/Krabbe/Krabbe.html".  
-----  
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-----  
CC EMBL; D25283; BAA04971.1; -  
CC EMBL; D25284; BAA04972.1; -  
CC EMBL; L23116; AAA16645.1; -  
CC EMBL; L38559; AAA80975.1; -  
CC EMBL; L38544; AAA80975.1; JOINED.  
CC EMBL; L38545; AAA80975.1; JOINED.  
CC EMBL; L38546; AAA80975.1; JOINED.  
CC EMBL; L38547; AAA80975.1; JOINED.  
CC EMBL; L38548; AAA80975.1; JOINED.  
CC EMBL; L38549; AAA80975.1; JOINED.  
CC EMBL; L38550; AAA80975.1; JOINED.  
CC EMBL; L38551; AAA80975.1; JOINED.  
CC EMBL; L38552; AAA80975.1; JOINED.  
CC EMBL; L38553; AAA80975.1; JOINED.  
CC EMBL; L38555; AAA80975.1; JOINED.  
CC EMBL; L38556; AAA80975.1; JOINED.  
CC EMBL; L38557; AAA80975.1; JOINED.  
CC EMBL; L38558; AAA80975.1; JOINED.

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DR EMBL; D86181; BAA24902.1; -.
DR EMBL; D84232; BAA24902.1; JOINED.
DR EMBL; D84233; BAA24902.1; JOINED.
DR EMBL; D84234; BAA24902.1; JOINED.

Query Match      13.7%; Score 63.5; DB 1; Length 669;
Best Local Similarity 23.5%; Pred. No. 43;
Matches 20; Conservative 15; Mismatches 43; Indels 7; Gaps 1;

QY 5 LSLILLVCEATWRNSGNTLENGYFLSRNKENHSQPTQSSLEDSTVTKAVKTTGKGI 64
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 LQVKIIASDNLMSIASMLLDALFKVVDVIGAHYPGTHSAKDA-----KLTGKKL 254
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 65 VKGNLDSRLGLIGABAGRGVKKV 89
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 255 WSEDFSTLNSDMGACGWRILNQ 279
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
CDC5 YEAST
ID CDC5 YEAST STANDARD; PRT; 705 AA.
AC P32562;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37).
GN CDC5 OR PKX2 OR MSP2 OR YMR001C OR YMR270.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RC STRAIN=A364A;
RX MEDLINE=93309479; PubMed=8321244;
RA Kitada K., Sugano A., Johnson L.H., Johnson A.L.;
RA "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
RT cycle mutant gene dbf4 encodes a protein kinase and is identified as
RT CDC5";
RL Mol. Cell. Biol. 13:4445-4457(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churche C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagers K., Lye G., Moulé S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrrell B.G.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
RN [3]
RP PHOSPHORYLATION OF SCCL.
RX MEDLINE=21264235; PubMed=11371343;
RA Alexandru G., Uhlmann F., Mechtler K., Poupert M.-A., Nasmyth K.;
RA "Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 Kinase
RT regulates sister chromatid separation in yeast.";
RL Cell 105:459-472(2001)
CC
CC -!- FUNCTION: Protein kinase required for the cell cycle.
CC Phosphorylates SCCL/MCD1.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC CDC5/Polo subfamily.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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DR EMBL; M84220; AAA02576.1; -.
DR EMBL; Z48613; CA888516.1; -.
DR EIR; A48144; A48144.
DR HSP; Q63450; IA06.
DR Germline; 142669; -.
DR SGD; S0004603; CDC5.
DR GO; GO:0005935; C:bud neck; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0000922; C:spindle pole; IDA.
DR GO; GO:0006268; P:DNA dependent DNA replication; IDA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser thr pkin AS.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00669; pkinase; 1.
DR Pfam; PF00659; POLO box; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS50078; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Cell cycle; Cell division; Serine/threonine-protein kinase;
KW Transferase; ATP-binding; Repeat.
FT DOMAIN 82 337 PROTEIN KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT_SITE 204 204 BY SIMILARITY.
FT DOMAIN 520 587 POLO BOX 1.
FT DOMAIN 619 692 POLO BOX 2.
FT SEQUENCE 705 AA; 81030 MW; B5A25F1BBBAA3DC CRC64;
SQ

Query Match      13.7%; Score 63.5; DB 1; Length 705;
Best Local Similarity 31.2%; Pred. No. 46;
Matches 15; Conservative 6; Mismatches 22; Indels 5; Gaps 1;

QY 32 LSRNKENHSQPTQSSLEDSTV-----TPTKAVKTTGKGI VKGRNLDSSG 74
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 45 LDPNDHHQHPAQKKREKLSALCKTPPSLIKTGRKDYHRRGFLGEGG 92
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
KEL2 YEAST
ID KEL2 YEAST STANDARD; PRT; 882 AA.
AC P50090;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kelch repeats protein 2.
GN KEL2 OR YGR238C OR G8585.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=96267763; PubMed=8701610;
RA van der Aart Q.J.M., Kleine K., Steensma H.Y.;
RA "Sequence analysis of the 43 kb CRM1-YLM9-PET54-DIE2-SMI1-PHO81-YHB4-
RT PKI region from the right arm of Saccharomyces cerevisiae chromosome
RT VII.";
RL Yeast 12:385-390(1996).
RN [2]
RN CHARACTERIZATION.
RP MEDLINE=99003296; PubMed=9786949;
RX Phillips J., Herskowitz I.;
RA "Identification of Kelp1, a kelch domain-containing protein involved
RT in cell fusion and morphology in Saccharomyces cerevisiae.";
RL J. Cell Biol. 143:375-389(1998).
RL
```

CC -!- SUBUNIT: Interacts with KELL.  
CC -!- SIMILARITY: Contains 4 Kelch repeats.  
CC -!- SIMILARITY: TO YEAST KELL AND S.POMBE SPAC6G10.02C.  
CC  
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CC  
CC EMBL; X87941; CAA61189.1; -  
CC EMBL; 273023; CAA97266.1; -  
CC PIR; S57704; S57704.  
CC GeneOnline; 141550; -  
CC SGD; S0003470; KELL2.  
CC GO; GO:0005935; C:bud neck; IDA.  
CC GO; GO:0005934; C:bud tip; IDA.  
CC GO; GO:0005937; C:shmoo tip; IDA.  
CC GO; GO:0000747; P:conjugation with cellular fusion; IGI.  
CC InterPro; IPR006652; Kelch\_rep.  
CC Pfam; PF01344; Kelch; 4.  
CC KW Kelch repeat; Repeat; Coiled coil.  
CC FT REPEAT 99 143 KELLCH 1.  
CC FT REPEAT 213 267 KELLCH 2.  
CC FT REPEAT 268 317 KELLCH 3.  
CC FT REPEAT 319 369 KELLCH 4.  
CC FT REPEAT 550 685 COILED COIL (POTENTIAL).  
CC FT DOMAIN 728 881 COILED COIL (POTENTIAL).  
CC FT MAIN 882 AA; 99974 MW; 63B9772FF017E6D9 CRC64;  
CC SQ SEQUENCE 882 AA; 99974 MW; 63B9772FF017E6D9 CRC64;  
Query Match 13.7%; Score 63.5; DB 1; Length 882;  
Best Local Similarity 20.8%; Pred. No. 59;  
Matches 26; Conservative 20; Mismatches 34; Indels 45; Gaps 4;  
QY 11 LVCEAIWRNSGNTLENGYFLSRNKHNSQPT-----Q 44  
DB 418 IMCESLHAGSFNSLSGGTPTSKSTESNQEIINILTPRPSKVLVSYNDIDEGAGSYS 477  
QY 45 SLLEDSVTPTKA-----VKTTGKGI-VKGRNLD-SRGLILGAEAWGRG 85  
DB 478 SALDDKAFERKSDREERKPKSQSVDSINKESPTGKIVKKNFPVLRLGLTVDSERYGSS 537  
QY 86 VKKNT 90  
DB 538 SYKDT 542  
RESULT 8  
DMS6 AGAAN STANDARD; PRT; 80 AA.  
AC O93226;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Dermaseptin AA-3-6 precursor.  
OS Agalychnis anae (Yellow-eye leaf frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Phyllomedusinae; Agalychnis.  
OC NCBI\_TaxID=75990;  
[1]  
RN SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RP TISSUE-Skin;  
RX MEDLINE=98449786; PubMed=9774745;  
RA Wechselberger C.;  
RL "Cloning of cDNAs encoding new peptides of the dermaseptin-family.";  
RL Biochim. Biophys. Acta 1388:279-283(1998).  
CC -!- FUNCTION: Possesses a potent antimicrobial activity against Gram-  
CC positive and Gram-negative bacteria. Probably acts by disturbing  
CC membrane functions with its amphipathic structure (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
CC Dermaseptin subfamily.  
CC  
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CC  
CC EMBL; AJ005188; CAA06425.1; -  
CC InterPro; IPR004275; Brevenin.  
CC Pfam; PF03032; Brevenin; 1.  
CC KW Amphibian defense peptide; Antibiotic; Multigene family;  
CC Cleavage on pair of basic residues; Amidation; Signal.  
CC SIGNAL 1 22 POTENTIAL.  
CC FT PROPEP 23 43 POTENTIAL.  
CC FT PEPTIDE 46 77 DERMASEPTIN AA-3-6.  
CC FT PROPEP 79 80 POTENTIAL.  
CC FT MOD\_RES 77 77 AMIDATION (G-78 PROVIDE AMIDE GROUP)  
CC FT (POTENTIAL)  
CC SQ SEQUENCE 80 AA; 8817 MW; DB13FD831E7E2140 CRC64;  
Query Match 13.6%; Score 63; DB 1; Length 80;  
Best Local Similarity 27.1%; Pred. No. 4.5;  
Matches 23; Conservative 12; Mismatches 32; Indels 18; Gaps 4;  
QY 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRNKHNSQPTQSLSDSVTPTKAVKIT 60  
DB 10 LVLFGLVLSLTCBEKKN-----EDEEQEDQSEMKKGMWST--IRNV 54  
QY 61 KGKGVKGRNLDGRGLILGA--EAWG 83  
DB 55 GKSRAKAANLPKA-ALGALISEAVG 78  
RESULT 9  
PYRF PACTA STANDARD; PRT; 268 AA.  
ID PYRF PACTA STANDARD; PRT; 268 AA.  
AC O93864;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)  
DE (OMPDCase) (OMPDCase) (Uridine 5'-monophosphate synthase) (UMP  
DE synthase).  
DE URA3.  
OS Pachysolen tannophilus (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Pachysolen.  
OC NCBI\_TaxID=4918;  
[1]  
RN SEQUENCE FROM N.A.  
RA Clark-Walker G.D.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).  
CC -!- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.  
CC -!- SIMILARITY: Belongs to the OMP decarboxylase family.  
CC  
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CC  
CC EMBL; AF047170; AAD02431.1; -  
CC HSP; P03962; IDOW.  
CC InterPro; IPR001754; OMPdecase.  
CC Pfam; PF00215; OMPdecase; 1.  
DR

```
DR PROSITE: PS00156; OMEDECASE; 1.
KW Pyrimidine biosynthesis; Lyase; Decarboxylase.
FT ACT SITE 95 BY SIMILARITY.
SQ SEQUENCE 268 AA; 29684 MW; ECC89602DA2FC10A CRC64;

Query Match 13.5%; Score 62.5; DB 1; Length 268;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 21; Conservative 8; Mismatches 23; Indels 21; Gaps 2;

QY 20 NSGSNTLNGYFLSRNKHNSPTQSSLEDSVTPKAVKTTGKIVKG-----RNLDLS 72
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 101 NTVKQYKNGIF-----KIAQWADIINAHGVTGEGIVKGLKEAALETTLFEP 146
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 73 RGLILGAERWGRG 85
   ||||| : | | | | |
Db 147 RGLILMIAELSSKG 159

RESULT 10
Y528 SYNY3
ID Y528.SYNY3 STANDARD; PRT; 379 AA.
AC Q55518;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein sl10528 (EC 3.4.24.-).
GN SLL0528.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96127529; PubMed=8590279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugita M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to peptidase family M50B.
CC -1- SIMILARITY: Contains 2 CBS domains.
CC -----
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CC -----
CC EMBL; D64006; BAA10876.1; -.
CC PIR; S76029; S76029.
CC MEROPS; M50.UPB; -.
CC InterPro; IPR000644; CBS domain.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR008915; Peptidase_M50.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF02163; Peptidase_M50; 1.
CC SMART; SM00116; CBS; 2.
CC DR DR
KW Hypothetical protein; Hydrolase; 1.
KW Repeat; CBS domain; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 260 310 CBS 1.
FT DOMAIN 327 375 CBS 2.
FT METAL 75 75 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 76 76 BY SIMILARITY.
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FT METAL 79 79 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 379 AA; 40465 MW; 1CC3251660078ECB CRC64;

Query Match 13.5%; Score 62.5; DB 1; Length 379;
Best Local Similarity 26.5%; Pred. No. 29;
Matches 22; Conservative 13; Mismatches 41; Indels 7; Gaps 1;

QY 5 LSLMLLLVCEAIRWSRNSGNTLNGYFLSRNKHNSPTQSSLEDSVTPKAVKTTGKI 64
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 211 LGLILNLPISGFWTILIGFWLLQAGSSARNAQVKEQMEAFDAEVIPIPSIIPAGLNI 270
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 -----VKGRNLDGRGLILGAE 80
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 271 REFANDYVIGKTPWRFRFLVIGAD 293

RESULT 11
DPOL METJA
ID DPOL.METJA STANDARD; PRT; 1634 AA.
AC Q58295;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
DE intein].
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii.";
RT Science 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N)
CC -1- PTM: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the intervening region (intein)
CC followed by peptide ligation (Potential).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67532; AAB98889.1; -.
CC HSP; P56689; ITG0.
CC TIGR; MJ0885; -.
CC InterPro; IPR006172; DNA_pol_B.
CC InterPro; IPR006134; DNA_pol_B_dom.
CC InterPro; IPR006133; DNA_pol_B-exo.
CC InterPro; IPR003587; Hedgehog hint_N.
CC InterPro; IPR003586; Hedgehog hint_C.
CC InterPro; IPR006142; INTEIN.
CC InterPro; IPR004042; Intein endonuc.
CC InterPro; IPR006141; Intein_S.
CC InterPro; IPR004578; Pol2.
CC Pfam; PF00136; DNA_pol_B; 3.
```

```
DR Pfam: PF03104; DNA pol B exo; 1.
DR PRINTS; PF00379; INTRIN.
DR SMART; SM00305; HintC; 2.
DR SMART; SM00306; HintN; 2.
DR SMART; SM00486; POLBc; 1.
DR TIGRFAMS; TIGR01443; intein_Cterm; 2.
DR TIGRFAMS; TIGR01445; intein_Nterm; 2.
DR TIGRFAMS; TIGR00592; POL2; 1.
DR PROSITE; PS00116; DNA POLYMERASE B; 1.
DR PROSITE; PS00818; INTEIN_C_TER; 2.
DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
DR PROSITE; PS00817; INTEIN_N_TER; 2.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Autocatalytic cleavage; Protein splicing;
KW Complete proteome.
FT CHAIN 1 425 POL, 1ST PART (POTENTIAL).
FT CHAIN 426 794 MJA POL-1 INTEIN (POTENTIAL).
FT CHAIN 795 882 POL, 2ND PART (POTENTIAL).
FT CHAIN 883 1358 MJA POL-2 INTEIN (POTENTIAL).
FT CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
FT CHAIN 1634 191708 MW; 84A1FAFAB1F97DDD CRC64;
SQ SEQUENCE 1634 AA; 191708 MW; 84A1FAFAB1F97DDD CRC64;

Query Match 13.4%; Score 62; DB 1; Length 1634;
Best Local Similarity 29.2%; Pred. No. 1.7e+02;
Matches 21; Conservative 9; Mismatches 24; Indels 18; Gaps 4;

QY 25 TLENGYFLSRKHNHSTQSSLEDSVT-----PTKAVKTTGKGVKGRNLSRGLI 76
Db 402 TYEGGV-----KEPEKGFEDIIISDFRCHPKTKV-VKGGVNIEDVKEGNYV 452
QY 77 LGAEAWGRGVKK 88
Db 453 LGIDGWQK-VKX 463

RESULT 12
TRM1 AERPE
ID TRM1 AERPE STANDARD; PRT; 401 AA.
AC Q9YDY;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32)
DE (tRNA(guanine-26,N(2)-N(2)) methyltransferase)
DE dimethylguanosine-26 methyltransferase)
DE (tRNA(m(2,G26)dimethyltransferase).
GN TRM1 OR AFE0782.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
CC -!- FUNCTION: Dimethylates a single guanine residue at position 26 of
CC a number of tRNAs using S-adenosyl-L-methionine as donor of the
CC methyl groups (By similarity).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-
CC homocysteine + tRNA containing N(2)-methylguanine.
CC -!- SIMILARITY: Belongs to the TRM1 family.
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-----
CC EMBL; AP000060; BAA79760.1; ALT_INIT.
CC HAMAP; MF_00290; -; 1.
CC InterPro; IPR002905; TRM.
CC Pfam; PF02005; TRM; 1.
CC TIGRFAMS; TIGR00308; TRM1; 1.
KW Transferase; Methyltransferase; Complete proteome.
SQ SEQUENCE 401 AA; 43034 MW; 570005B39E83366E CRC64;

Query Match 13.3%; Score 61.5; DB 1; Length 401;
Best Local Similarity 29.9%; Pred. No. 40;
Matches 23; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY 20 NGSNTLENGYFLSRKHNHSTQSSLEDSVT-----PTKAVKTTGKGVKGRNLSRGLI 64
Db 105 NARANGLEFGSYMIFNKESNLMFHLRERPTFVSLIDIDPYGSPAPFVDALALSGKGT 164
QY 65 VKGRNLSRGLILGAEA 81
Db 165 VVAMTATDLAVLEGGA 181

RESULT 13
MEFA XENLA
ID MEFA XENLA STANDARD; PRT; 516 AA.
AC Q03414;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myocyte-specific enhancer factor 2A homolog (serum response factor-
DE like protein 2) (SL-2).
GN MEF2A OR SL2.
OS Xenopus laevis (African clawed frog).
OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neurula;
RX MEDLINE=9309873; PubMed=1281451;
RA Chambers A.E., Kotecha S., Towers N., Mohun T.J.;
RA "Muscle-specific expression of SRF-related genes in the early embryo
of Xenopus laevis."
RT EMBO J. 11:4981-4991(1992).
RL -!- FUNCTION: MAY REGULATE MUSCLE-SPECIFIC TRANSCRIPTION IN THE
CC EMBRYO AND MAY REGULATE TRANSCRIPTION OF A VARIETY OF CELL TYPES
CC IN THE ADULT. IT BINDS TO THE SEQUENCE CTA(T/A)ATAT.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: RESTRICTED TO THE SOMITIC MESODERM OF EARLY
CC EMBRYOS AND TO THE BODY MUSCLE (MYOTOMES) OF THE TADPOLE.
CC EXPRESSED IN ALL TISSUES EXAMINED IN THE ADULT.
CC -!- DEVELOPMENTAL STAGE: Expression begins in the early neurula.
CC -!- SIMILARITY: Belongs to the MEF2 family.
CC -!- SIMILARITY: Contains 1 MADS-box domain.
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CC or send an email to license@isb-sib.ch)
-----
CC EMBL; Z19123; CAA79530.1; -
CC PIR; S28060; S28060.
CC HSSP; P11831; 1SR5.
CC TRANSFAC; T01784; -
```



Mon Apr 5 12:02:01 2004

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EMBL; Z49259; CAA89232.1; -.  
 PIR; S54461; S54461.  
 GerMOnline; 142754; -.  
 SGD; S0004692; YMR086W.  
 Hypothetical protein.  
 SEQUENCE 960 AA; 105873 MW; 05AAFA27129D809B CRC64;

```
Query Match      13.3%; Score 61.5; DB 1; Length 960;
Best Local Similarity 36.2%; Pred. No. 1.1e+02;
Matches 21; Conservative 10; Mismatches 20; Indels 7; Gaps 3;
```

QY 18 RNSGSGNTL--ENGVELSR---NKENHSQPQTQSSLEDVSTPTKAVTGTGKIVKGRNL 70  
||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
b6 214 RNSAHSALNARNGSILRKVKVSQESLSHQPCKTSSLGNSTSTQAKK--GQKAVQERNL 269

Search completed: March 31, 2004, 12:14:02  
Job time : 15 secs



Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	70	15.2	256	2	AE1736	anti-repressor hom	
2	68.5	14.8	495	2	S79697	hypothetical prote	
3	68	14.8	622	2	A83459	transferrin recept	
4	68.5	14.7	280	2	E82099	phosphatidate cyti	
5	68	14.7	1334	2	A41524	rho1 gdp-gtp excha	
6	66.5	14.4	337	2	A81026	hypothetical prote	
7	66.5	14.4	479	1	S41015	transcription fact	
8	66	14.3	851	2	T47495	hypothetical prote	
9	65	14.1	313	2	A82436	transcription regu	
10	65	14.1	360	2	H97313	protein distantl	
11	65	14.1	368	2	S36576	E2 protein - human	
12	65	14.1	379	2	T24654	hypothetical prote	
13	64.5	14.0	532	2	T06029	hypothetical prote	
14	64	13.9	257	2	A11442	anti-repressor (Ba	
15	64	13.9	430	2	T46099	hypothetical prote	
16	64	13.9	548	2	T28910	hypothetical prote	
17	63.5	13.7	598	2	A64594	site-specific DNA-	
18	63.5	13.7	651	2	A96781	unknown protein. F9	
19	63.5	13.7	669	2	I54205	galactosylceramida	
20	63.5	13.7	705	2	A48144	protein kinase CDC	
21	63.5	13.7	850	2	T14472	S-receptor kinase	
22	63.5	13.7	882	2	S57704	hypothetical prote	
23	63	13.6	249	2	T00169	anti-repressor - S	
24	63	13.6	250	2	H89889	anti-repressor (im	
25	63	13.6	441	2	F86185	hypothetical prote	
26	63	13.6	457	2	E96572	protein F12M16.8 [	
27	63	13.6	2425	2	D69426	surface layer prote	
28	62.5	13.5	379	2	S76029	hypothetical prote	
29	62.5	13.5	381	2	T19402	hypothetical prote	

A;Cross-references: EMBL:D64005; GB:AB001339; NID:G100179; FIDN:BAH0035:I; IIS:



[illegible]

A;Reference number: S36469  
A;Accession: S36576  
A;Molecule type: DNA  
A;Residues: 1-368 <DEL>  
A;Cross-references: EMBL:X74481; NID:g397038; PIDN:CAAS2588.1; PID:g397042  
C;Superfamily: papillomavirus E2 protein  
C;Keywords: DNA binding, early protein; transcription regulation

Query Match 14.1%; Score 65; DB 2; Length 368;  
Best Local Similarity 27.0%; Pred. No. 29;  
Matches 24; Conservative 11; Mismatches 40; Indels 14; Gaps 3;

QY 10 LLLVCEAIWRSNGSNTLENGYFLSRN-----KENHSOPTQSSLEDSVTPTKAVK 58  
Db 192 VIVCPASVSNEVSTT-ETAVHLCTETSKTSVAVGAKDTHLQPPQRRRPDVDSRNTK 250  
QY 59 TTGKGIVKGNLDS--RGILGAEAWGRG 85  
Db 251 YPNLLRGQSQVSDTTRGLVTATECTNKG 279

RESULT 12  
T24654  
hypothetical protein T07D10.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C;Accession: T24654  
R;White, S.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19918  
A;Accession: T24654  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-379 <WIL>  
A;Cross-references: EMBL:Z81588; PIDN:CAB04712.1; GSPDB:GN00019; CESP:T07D10.2  
A;Experimental source: clone T07D10  
C;Genetics:  
A;Gene: CESP:T07D10.2  
A;Map position: 1  
A;Introns: 37/3; 85/3; 271/1; 319/1  
C;Superfamily: oxytocin receptor

Query Match 14.1%; Score 65; DB 2; Length 379;  
Best Local Similarity 35.9%; Pred. No. 30;  
Matches 14; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 8 LLLLVCEAIWRSNGSNTLENGYFLSRNKHHSOPTQSS 46  
Db 228 LYLVCCKAVWKSTSFSSSLRN----NMKKMEHMKLTEKN 262

RESULT 13  
T06029  
hypothetical protein T28I19.100 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 22-Oct-1999  
C;Accession: T06029  
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba  
submitted to the Protein Sequence Database, March 1999  
A;Reference number: Z15484  
A;Accession: T06029  
A;Molecule type: DNA  
A;Residues: 1-532 <BEV>  
A;Cross-references: EMBL:AL035709; GSPDB:GN00062; ATSP:T28I19.100  
A;Experimental source: cultivar Columbia; BAC clone T28I19  
C;Genetics:  
A;Gene: ATSP:T28I19.100  
A;Map position: 4

Query Match 14.0%; Score 64.5; DB 2; Length 532;  
Best Local Similarity 34.7%; Pred. No. 50;  
Matches 17; Conservative 9; Mismatches 18; Indels 5; Gaps 1;

QY 14 EAINESNGSNTLENGYFLSRNKHHSOPTQSSLEDSVTPTKAVTKTG 62  
Db 274 ESSGDSGSGKSTGYQOTKNEDEKVKQSSSEES-----KVESGK 317

RESULT 14  
A11442  
anti-repressor (Bacteriophage A118) homolog lin0080 [imported] - Listeria innocua (st.  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: A11442  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi,  
D.; Jones, L.M.; Karst, U  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuraphat, G.; Madueno, E.; Maitournam, A.;  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan  
A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: A11442  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-257 <GLA>  
A;Cross-references: GB:ALS92022; PIDN:CAC95313.1; PID:g16412500; GSPDB:GN00178  
A;Experimental source: strain Clip11262  
C;Genetics:  
A;Gene: lin0080

Query Match 13.9%; Score 64; DB 2; Length 257;  
Best Local Similarity 29.4%; Pred. No. 25;  
Matches 15; Conservative 8; Mismatches 14; Indels 14; Gaps 1;

QY 27 ENGYSLSRNKHHSOPTQSSLEDSVTPTK-----AVKTTGKG 63  
Db 191 QRGYLIRKGTIDYNRPTQKSMELGLFKIKETAIIRSSGQTAITAKVTGK 241

RESULT 15  
T46099  
hypothetical protein T25B15.60 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 06-Oct-2000  
C;Accession: T46099  
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer,  
submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23021  
A;Accession: T46099  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-430 <ALC>  
A;Cross-references: EMBL:AL132972  
A;Experimental source: cultivar Columbia; BAC clone T25B15  
C;Genetics:  
A;Map position: 3  
A;Introns: 23/3; 122/3; 194/3; 234/3  
A;Note: T25B15.60  
C;Superfamily: Arabidopsis thaliana hypothetical protein T16L24.240

Query Match 13.9%; Score 64; DB 2; Length 430;  
Best Local Similarity 27.4%; Pred. No. 45;  
Matches 20; Conservative 14; Mismatches 23; Indels 16; Gaps 3;

QY 17 WRSNS--GSNT-----LENGYFLSRNKHHSOPTQSSLEDSVTPTKAVTKTG 61  
Db 237 WKNSTKMGSTFMDPNPNHGWHSWLER-WWAAPNENHSUTPDNAEKDSSARSVASRAMS 295

QY 62 KGIVKGNLDSRG 74  
Db 296 EMIPRGKNLSPRG 308

Search completed: March 31, 2004, 12:15:28  
Job time : 22 secs



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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:12:31 ; Search time 23 Seconds  
(without alignments)  
202.015 Million cell updates/sec

Title: US-09-989-293A-377  
Perfect score: 462  
Sequence: 1 MTFLLSLLLLLVCEAIRNSN.....DSRGLILGAEANGRGVKKNT 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A-COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B-COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A-COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PTUS-COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	143.5	31.1	244	3	US-08-772-440-2
2	139.5	30.2	50	3	US-08-772-440-25
3	139.5	30.2	176	3	US-08-772-440-8
4	128.5	27.8	180	3	US-08-772-440-31
5	69.5	15.0	171	4	US-09-205-258-481
6	69.5	15.0	257	4	US-09-205-258-421
7	68.5	14.8	622	1	US-08-547-197-1
8	68.5	14.8	622	3	US-08-957-940-1
9	66.5	14.4	354	4	US-09-252-991A-32891
10	65.5	14.2	247	4	US-09-134-000C-6345
11	65	14.1	461	4	US-09-134-001C-3604
12	64	13.9	126	4	US-09-198-452A-1254
13	63.5	13.7	317	4	US-09-594-506-30
14	63.5	13.7	881	4	US-09-489-039A-12003
15	63	13.6	315	4	US-09-134-001C-4255
16	62	13.4	1017	4	US-09-762-724-12
17	62	13.4	1023	4	US-09-762-724-14
18	62	13.4	1027	4	US-09-762-724-8
19	61.5	13.3	789	3	US-08-960-780-6
20	61.5	13.3	789	3	US-08-073-898-6
21	61.5	13.3	789	4	US-09-002-285-90
22	61.5	13.3	789	4	US-09-589-477-90
23	61.5	13.3	789	4	US-09-850-351A-6
24	61	13.2	237	3	US-08-808-148-3
25	61	13.2	237	4	US-08-976-594-216
26	61	13.2	254	4	US-09-252-991A-21292
27	60	13.0	217	4	US-09-107-532A-6400

28	60	13.0	1029	4	US-09-762-724-6	Sequence 6, Appli
29	59.5	12.9	237	4	US-09-252-991A-26577	Sequence 26577, A
30	59.5	12.9	921	4	US-09-543-681A-5734	Sequence 5734, Ap
31	59	12.8	415	4	US-03-252-991A-31892	Sequence 31892, A
32	59	12.8	641	3	US-08-836-567-10	Sequence 10, Appl
33	59	12.8	641	4	US-09-606-304-10	Sequence 4, Appli
34	59	12.8	1742	4	US-09-386-962C-4	Sequence 2, Appli
35	59	12.8	3623	4	US-09-341-461-2	Sequence 5, Appli
36	58.5	12.7	418	3	US-08-030-267-5	Sequence 8, Appli
37	58.5	12.7	924	3	US-08-619-812-8	Sequence 2, Appli
38	58.5	12.7	926	1	US-07-908-253-2	Sequence 2, Appli
39	58.5	12.7	926	1	US-08-455-970A-2	Sequence 2, Appli
40	58.5	12.7	926	1	US-08-387-156-6	Sequence 6, Appli
41	58.5	12.7	926	2	US-08-694-865-6	Sequence 6, Appli
42	58.5	12.7	926	2	US-08-878-748-6	Sequence 2, Appli
43	58.5	12.7	926	2	US-08-535-837-2	Sequence 2, Appli
44	58.5	12.7	926	3	US-08-124-431-6	Sequence 6, Appli
45	58.5	12.7	926	4	US-09-383-912-6	Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-08-772-440-2  
; Sequence 2, Application US/08772440  
; Patent No. 6046158  
; GENERAL INFORMATION:  
; APPLICANT: Arizumi, Kiyoshi  
; APPLICANT: Takashima, Akira  
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/772,440  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTDX:493  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-772-440-2

Query Match 31.1%; Score 143.5; DB 3; Length 244;  
Best Local Similarity 61.7%; Pred. No. 7.6e-10;  
Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;  
Qy 15 AIWRNSGNTLENGVLSNKENHSQPTOSLSLDSVTPTKAVKTTG 61  
Db 68 AFWRHNSGRNPFKNFLSRNKNH-KPTESLSLDEKVAKSCQTIG 113

```

RESULT 2
US-08-772-440-25
; Sequence 25, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-772-440-25

Query Match 30.2%; Score 139.5; DB 3; Length 50;
Best Local Similarity 62.2%; Pred. No. 2.6e-10;
Matches 28; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 17 WRNSGSGNTLENGYFLSRNKENHSQPTQSSLEDSVTETKAVKTTG 61
Db 2 WRHNSGRNPBEKONFLSRNKENH-KPTESLSLDEKVAFSKASQTTG 45

RESULT 3
US-08-772-440-8
; Sequence 8, Application US/08772440
; Patent No. 6046158
; GENERAL INFORMATION:
; APPLICANT: Ariizumi, Kiyoshi
; APPLICANT: Takashima, Akira
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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Best Local Similarity 62.8%; Pred. No. 3.7e-08;
Matches 27; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 19 SNSGNTLNGYFLSRNKENHSQTSLSLEDSVTPTKAVKTTG 61
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 8 SNSGRNPEKDFLSRKNENH-KPTLESSLDERKVPKASQTG 49

RESULT 5
US-09-205-258-481
; Sequence 481, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 481
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (159)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals stop translation
; US-09-205-258-481

Query Match 15.0%; Score 69.5; DB 4; Length 171;
Best Local Similarity 31.8%; Pred. No. 0.8;
Matches 21; Conservative 14; Mismatches 22; Indels 9; Gaps 2;

QY 5 LSLILLVCEA---IWRNSGNTLNGYFLSRN-----KENHSQTSLSLEDSVTPTK 55
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 25 LVALLLVSAALSSVSVSRDPSPTVLNHSITPNVNALTHEQTKEPSISQISTLTLPPTI 84
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 56 AVKTTG 61
    :|||:
Db 85 STKKG 90

RESULT 6
US-09-205-258-421
; Sequence 421, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,890
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; SEQ ID NO 421
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-421

Query Match      15.0%; Score 69.5; DB 4; Length 257;
Best Local Similarity 31.8%; Pred. No. 1.4;
Matches 21; Conservative 14; Mismatches 22; Indels 9; Gaps 2;

QY 5 LSLLLLVCEA-----IWRNSGNSVLENGYFLSRN-----KENHSQPTOSLSLDSVTPTK 55
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 LVLALLNSAALS SVVSRDTSPTVLASHSTPNVNLTHENQTRKPSISQISTILPPTT 84
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 AVKTTG 61
   : : : : :
Db 85 STKSG 90
   : : : : :

RESULT 7
US-08-547-197-1
; Sequence 1, Application US/08547197
; Patent No. 5691157
; GENERAL INFORMATION:
; APPLICANT: Gong, Joseph K.
; APPLICANT: Glowski, Chester A.
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/547,197
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rogalsky, Peter
; REGISTRATION NUMBER: 38,601
; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1634
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-547-197-1

Query Match      14.8%; Score 68.5; DB 1; Length 622;
Best Local Similarity 27.6%; Pred. No. 6.4;
Matches 21; Conservative 15; Mismatches 23; Indels 17; Gaps 3;

QY 32 LSRNKENHSQPT---QSSLEDSVTPTKAVKTTGK-----GIVKGRNLDSRGLI 76
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 207 LFKMNEGNCPPSWIDSSCKLELSONQNVKLTVNNVLKETRLNIFGVKIKSEEDRIV 266
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 77 LGA--EAWGRGVKXNT 90
   : : : : :
Db 267 VQAQDANGPGVAKSS 282
   : : : : :
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
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Mon Apr 5 12:01:58 2004

RESULT 8  
US-08-957-940-1  
; Sequence 1, Application US/08957940  
; Patent No. 6132981  
; GENERAL INFORMATION:  
; APPLICANT: Gong, Joseph K.  
; APPLICANT: Glomski, Chester A.  
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR  
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/957,940  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/547,197  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rogalsky, Peter  
; REGISTRATION NUMBER: 38,601  
; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1634  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 622 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-957-940-1  
  
Query Match 14.8%; Score 68.5; DB 3; Length 622;  
Best Local Similarity 27.6%; Pred. No. 6.4;  
Matches 21; Conservative 15; Mismatches 23; Indels 17; Gaps 3;  
  
Qy 32 LSRNKHNSQPT---QSSLEDSVPTTKAVKTKG-----GIVKGNLDSRLGI 76  
Db 207 LFKMNEGCPSPWIDSKLELSONQNVKLTNNVLKTRILNIFGVKIGYEPRDRIY 265  
Qy 77 LGA--EAWGRGVKXNT 90  
Db 267 VGAQRDANGPGVAKSS 282  
  
RESULT 9  
US-09-252-991A-32891  
; Sequence 32891, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 32891  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-32891  
  
Query Match 14.4%; Score 66.5; DB 4; Length 354;  
Best Local Similarity 25.7%; Pred. No. 5.2;  
Matches 19; Conservative 12; Mismatches 32; Indels 11; Gaps 2;  
  
Qy 15 AIWRNSGNTLENGYFLSRNKHNSQPTQSSLEDSVPT-----KAVKTKGIV 65  
Db 72 ALWTVSDRDD--DRYLRLQPSAEGSDQFWQAESEFIAPTPDPSGLPQWGMSTRVWLSGLV 129  
Qy 66 KGRNLDSEGLIIGA 79  
Db 130 RGNLDFEGIACDA 143  
  
RESULT 10  
US-09-134-000C-6345  
; Sequence 6345, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 6345  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-6345  
  
Query Match 14.2%; Score 65.5; DB 4; Length 247;  
Best Local Similarity 30.8%; Pred. No. 4.2;  
Matches 16; Conservative 7; Mismatches 14; Indels 15; Gaps 1;  
  
Qy 27 ENGYFLSRNKHNSQPTQSSL-----EDSVPTTKAVKTKG 63  
Db 185 EKGILKRGKTDWNPQKSMQMDLELFVETIARSDGVSISKTPKVTCKG 236  
  
RESULT 11  
US-09-134-001C-3604  
; Sequence 3604, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3604  
; LENGTH: 461  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3604

```
Query Match      14.1%; Score 65; DB 4; Length 461;
Best Local Similarity 29.5%; Pred. No. 12;
Matches 18; Conservative 10; Mismatches 19; Indels 14; Gaps 3;

QY 23 SNTLENGY-FLSRN-----KENH-----SPTQSSLEDSVPTKAVKTKGKIVKGR 68
DB 83 SNVHPGVFLSESTNFAKAVEDNHHFPGSKTTWMMGDKITARQIVKQAGVPVPGS 142

QY 69 N 69
DB 143 N 143

RESULT 12
US-09-198-452A-1254
; Sequence 1254, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1254
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1254

Query Match      13.9%; Score 64; DB 4; Length 126;
Best Local Similarity 24.8%; Pred. No. 2.5;
Matches 25; Conservative 14; Mismatches 30; Indels 32; Gaps 4;

QY 6 SLLLLVCEAIRWSNGSNTLENGYFLSRN---KENHSQP-----TQSSLEDSVT 52
DB 15 AICLASICKV-----SSRFLSNINFKNTTTPREIVLPNPOTMSALNPEIT 63

QY 53 P-----TKAVKTKGKIVKGRNLDRLGLILGAEAWGRG 85
DB 64 PLSTIAPQTRRPTTKVIPRARDLLSLGITNFVSSGGVG 104

RESULT 13
US-09-594-506-30
; Sequence 30, Application US/09594506
; Patent No. 6512164
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: Thiamine Biosynthetic Enzymes
; FILE REFERENCE: BB1372 US NA
; CURRENT APPLICATION NUMBER: US/09/594,506
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,556
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-594-506-30

Query Match      13.7%; Score 63.5; DB 4; Length 317;
Best Local Similarity 24.2%; Pred. No. 11;
Matches 23; Conservative 20; Mismatches 33; Indels 19; Gaps 4;

QY 10 LIVCEAIRWSNGSNTLENGYFLSRNKHNSQPTQSSLEDSVPTKAV-----KT 59
DB 163 VVVEDLVVKEHRTGVVTINWALVSNQDTHSQ-TQSHMDANVMEAKIVVSSCGHGLFSA 221
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QY 60 TGKGVKGRNLDRLGLI-----LGAEAWGRGVKKN 89
DB 222 NGKGV---KRLDGLMIKTVPTGNEALDINVSED 253

RESULT 14
US-09-489-039A-12003
; Sequence 12003, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12003
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12003

Query Match      13.7%; Score 63.5; DB 4; Length 881;
Best Local Similarity 29.9%; Pred. No. 44;
Matches 20; Conservative 7; Mismatches 29; Indels 11; Gaps 2;

QY 17 WRSNSGNTLENGYFLSRNKHNSQPTQSSLEDSVPTKAVKTKGKIVKGRNLD---R 73
DB 234 WSYSSGGSTSSN-----ENRWQVNSWLERDITPLRSRLTLGDSYTNQGVDFDGINFR 285

QY 74 GLILGAE 80
DB 286 GAQLASD 292

RESULT 15
US-09-134-001C-4255
; Sequence 4255, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4255
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4255

Query Match      13.6%; Score 63; DB 4; Length 315;
Best Local Similarity 28.6%; Pred. No. 12;
Matches 22; Conservative 12; Mismatches 35; Indels 8; Gaps 2;

QY 12 VCEAIRWSNGSNTLENGYFLSRNKHNSQPTQSSLEDSVPT---KAVKTKGKIVKGRN 69
DB 146 VIDPWLAKSGDSLMD-----ENTKNHLQSLTLLPLADVVTNPIPEAEITGKINDEES 199

QY 70 LDSGLILGAEAWGRGV 86
DB 200 IRKAGQIFINEIGSKGV 216
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Mon Apr 5 12:01:58 2004

us-09-989-293a-377.rai

Page 7

Search completed: March 31, 2004, 12:16:02  
Job time : 24 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:11:11 ; Search time 39 Seconds  
(without alignments)  
728.119 Million cell updates/sec

Title: US-09-989-293A-377  
Perfect score: 462  
Sequence: 1 MTFLLSLLLVCEAIWRSN.....DSRGLILGAEAWGRGVKKNT 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	247.5	53.6	189	4 Q96DR9	Q96dr9 homo sapien
2	247.5	53.6	192	4 Q96PA5	Q96pa5 homo sapien
3	247.5	53.6	247	4 Q9BXN2	Q9bxn2 homo sapien
4	217.5	47.1	247	6 Q8H2R8	Q8h2r8 macaca mula
5	143.5	31.1	244	11 Q9J750	Q9ji50 mus musculus
6	136.5	29.5	244	11 Q8K1L4	Q8k1l4 mus musculus
7	80	17.3	239	16 Q8NZP4	Q8nzp4 streptococc
8	80	17.3	242	16 Q938N5	Q938n5 streptococc
9	78	16.9	238	9 Q48391	Q48391 streptococc
10	77	16.7	287	9 Q38585	Q38585 streptococc
11	75	16.2	217	10 Q8S2U4	Q8s2u4 medicago sa
12	71	15.4	213	10 Q9SBR7	Q9sbr7 medicago va
13	70	15.2	205	16 Q8PDR9	Q8pdr9 xanthomonas
14	70	15.2	256	16 Q928W4	Q928w4 listeria in
15	70	15.2	661	5 Q9VG84	Q9vg84 drosophila
16	70	15.2	696	5 Q8MZC0	Q8mzc0 drosophila

17	69.5	15.0	265	4 Q8NC54	Q8nc54 homo sapien
18	69.5	15.0	265	4 Q9NRG2	Q9nrg2 homo sapien
19	68.5	14.8	495	16 Q55897	Q55897 synechocyst
20	68.5	14.8	498	13 Q93291	Q93291 fugu rubrip
21	68	14.7	280	16 Q9KPV7	Q9kpv7 vibrio chol
22	68	14.7	1008	16 Q9FA78	Q9fa78 leptospira
23	68	14.7	1334	3 Q9Y7U6	Q9y7u6 schistosacch
24	67.5	14.6	417	10 Q8LAR3	Q8lar3 arabidopsis
25	67	14.5	150	11 Q9D851	Q9d851 mus musculu
26	67	14.5	321	11 Q8BTR4	Q8btr4 mus musculu
27	67	14.5	356	13 Q57435	Q57435 fugu rubrip
28	67	14.5	975	5 Q862D2	Q862d2 drosophila
29	67	14.5	976	5 Q8INT1	Q8int1 drosophila
30	66.5	14.4	337	16 Q9HUJ9	Q9hu9 pseudomonas
31	66.5	14.4	602	10 Q8W3H4	Q8w3h4 oryza sativ
32	66.5	14.4	602	10 Q7XBV7	Q7xbv7 oryza sativ
33	66	14.3	145	12 Q8AZ84	Q8az84 influenza a
34	66	14.3	145	12 Q8AZ83	Q8az83 influenza a
35	66	14.3	145	12 Q8AZ82	Q8az82 influenza a
36	66	14.3	145	12 Q8AZ81	Q8az81 influenza a
37	66	14.3	145	12 Q8AZ80	Q8az80 influenza a
38	66	14.3	260	12 Q919W1	Q919w1 influenza a
39	66	14.3	417	10 Q9SFE3	Q9sef3 arabidopsis
40	66	14.3	491	12 Q919W0	Q919w0 influenza a
41	66	14.3	491	12 Q919W2	Q919w2 influenza a
42	66	14.3	498	12 Q9YIL3	Q9yil3 influenza a
43	66	14.3	498	12 Q9QNB5	Q9qnb5 influenzavi
44	66	14.3	498	12 Q8QM08	Q8qm08 influenza a
45	66	14.3	498	12 Q9QNB4	Q9qnb4 influenzavi

ALIGNMENTS

RESULT 1

Q96DR9 PRELIMINARY; PRT; 189 AA.  
AC Q96DR9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Beta-glucan receptor isoform C.  
GN BGR.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood leukocytes;  
RA Willment J.A., Gordon S., Brown G.D.;  
RT "Characterization of the human beta-glucan receptor and its  
alternatively spliced isoforms";  
RL J. Biol. Chem. 0:0-0(2001).  
DR EMBL; AF400597; AAL1713.1;  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
SQ SEQUENCE. 189 AA; 21065 MW; F7DF9F76EA4B6B59 CRC64;

Query Match 53.6%; Score 247.5; DB 4; Length 189;  
Best Local Similarity 80.6%; Pred. No. 5.8e-19;  
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

Qy	5	LSLILLVC-----EAIWRSNGSNTLENGYFLSRKNENHSQPTQSSLEDSVPTTKAVKT 59
Db	53	LCILVILVAVLGTMAIWRNSGNTLENGYFLSRKNENHSQPTQSSLEDSVPTTKAVKT 112
Qy	60	TG 61
Db	113	TG 114

RESULT 2

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Q96PA5
ID Q96PA5 PRELIMINARY; PRT; 192 AA.
AC Q96PA5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Beta-glucan receptor isoform G.
GN BGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta-glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF400601; AAL11717.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR SMART; SMART00034; SMART; 1.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR LECTIN; LECTIN.
SQ SEQUENCE 192 AA; 21130 MW; 6F3350B1DFBEC921 CRC64;

Query Match 53.6%; Score 247.5; DB 4; Length 192;
Best Local Similarity 80.6%; Pred. No. 5.9e-19;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 5 LSLALLLVC-----EAIWRSNGSNTLENGYFLSRNKHNSQTSLSDSVTPKAVKT 59
Db LCLVILVIAVLGTMAIWRSGSNTLENGYFLSRNKHNSQTSLSDSVTPKAVKT 112
QY 60 TG 61
Db 113 TG 114

RESULT 3
Q9BXN2 PRELIMINARY; PRT; 247 AA.
ID Q9BXN2;
AC Q9BXN2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dendritic cell-associated C-type lectin-1 (DECTIN-1 receptor) (Lectin-
DE like receptor 1) (Beta-glucan receptor isoform A).
GN DECTIN-1 OR DECTIN1 OR BGR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;
RT "Identification of a human homologue of the dendritic cell-associated
RT C-type lectin-1, dectin-1.";
RL Gene 272:51-60(2001).
RN [2]
SEQUENCE FROM N.A.
RA Sobanov Y., Bernreiter A., Dardak S., Mechtcheriakova D., Duechler M.,
RA Kalthoff F., Hofer E.;
RT "A novel cluster of lectin-like receptor genes expressed in monocytic,
RT dendritic and endothelial cells maps close to the NK receptor genes in
RT the human NK gene complex.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RX MEDLINE=21383615; PubMed=11491532;
RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;
RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene
RT expressed on dendritic cells.";
RL Immunogenetics 53:288-295(2001).
RN [4]
```

```
RP SEQUENCE FROM N.A.
RA Herranz-Falcon P., Arce I., Fernandez-Ruiz E.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood leukocytes;
RA Willment J.A., Gordon S., Brown G.D.;
RT "Characterization of the human beta-glucan receptor and its
RT alternatively spliced isoforms.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF313468; AAK37473.1; -.
DR EMBL; AJ312373; CAC43847.1; -.
DR EMBL; AY026769; AAK20114.2; -.
DR EMBL; AF400595; AAL11711.1; -.
DR Genew; HGNC:14558; CLECSF12.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c. 1.
DR PRINTS; PR00356; ANTIREEZEII.
DR SMART; SMART00034; SMART; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR LECTIN; LECTIN.
SQ SEQUENCE 247 AA; 27627 MW; 98393E3697611B9 CRC64;

Query Match 53.6%; Score 247.5; DB 4; Length 247;
Best Local Similarity 80.6%; Pred. No. 8.1e-19;
Matches 50; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 5 LSLALLLVC-----EAIWRSNGSNTLENGYFLSRNKHNSQTSLSDSVTPKAVKT 59
Db LCLVILVIAVLGTMAIWRSGSNTLENGYFLSRNKHNSQTSLSDSVTPKAVKT 112
QY 60 TG 61
Db 113 TG 114

RESULT 4
Q8HZR8 PRELIMINARY; PRT; 247 AA.
ID Q8HZR8;
AC Q8HZR8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Dendritic cell-associated C-type lectin-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
SEQUENCE FROM N.A.
RA Choi Y.K., Fallert B.A., Murphey-Corb M.A., Reinhart T.A.;
RT "Simian Immunodeficiency Virus Dramatically Alters Expression of
RT Homeostatic Chemokines and Dendritic Cell Markers during Infection In
RT Vivo.";
RL Blood 0:0-0(2002).
DR EMBL; AF508729; AAN47097.1; -.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR InterPro; IPR002353; AntifreezeII.
DR InterPro; IPR001304; Lectin C.
DR Pfam; PF00059; lectin c. 1.
DR PRINTS; PR00356; ANTIREEZEII.
DR SMART; SMART00034; SMART; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR LECTIN; LECTIN.
SQ SEQUENCE 247 AA; 27648 MW; 9DF0D86DF2461518 CRC64;

Query Match 47.1%; Score 217.5; DB 6; Length 247;
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Best Local Similarity 71.0%; Pred. No. 1.5e-15;  
Matches 44; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 5 LSLILLVLC-----EATWRSNGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKT 59  
DB 53 LCLVILVAVLVGHWAIWRPNSGRNSLENGYFSPENKENHSQPTQSPLEESVTPTKAVKT 112

QY 60 TG 61

DB 113 TG 114

RESULT 5

Q9J150 ID Q9J150 PRELIMINARY; PRT; 244 AA.  
AC Q9J150;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Dendritic cell-associated C-type lectin-1.  
GN CLECSF12 OR DECTIN-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RX MEDLINE=20347934; PubMed=10779524;  
RA Arizumi K., Shen G.-L., Shikano S., Xu S., Ritter R. III,  
RA Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;  
RT "Identification of a novel, dendritic cell-associated molecule,  
RT dectin-1, by subtractive cDNA cloning.";  
RL J. Biol. Chem. 275:20157-20167(2000).  
DR EMBL; AF262985; AAF72710.1; --  
DR MGD; MGI:1861431; Clecsf12.  
DR GO; GO:0005529; F.sugar binding; IEA.  
DR GO; GO:0007157; P.heterophilic cell adhesion; IEA.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT\_1.  
DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
DR Lectin.  
KW SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;  
SQ SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;

Query Match 31.1%; Score 143.5; DB 11; Length 244;  
Best Local Similarity 61.7%; Pred. No. 1.8e-07;  
Matches 29; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

QY 15 AIWRSNGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTG 61

DB 68 AFWRHNGRNPEKDNFLSRNKENH-KPTSSSLDEKVPASQTTG 113

RESULT 6

Q8K1L4 ID Q8K1L4 PRELIMINARY; PRT; 244 AA.  
AC Q8K1L4;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Similar to C-type (calcium dependent, carbohydrate recognition domain)  
DE lectin, superfamily member 12.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC027742; AAH27742.1; --  
DR GO; GO:0005529; F.sugar binding; IEA.

DR InterPro; IPR002353; AntifreezeII.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF00059; lectin\_c; 1.  
DR PRINTS; PR00356; ANTIFREEZEII.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
SQ SEQUENCE 244 AA; 27542 MW; F50158025FA80C2A CRC64;

Query Match 29.5%; Score 136.5; DB 11; Length 244;  
Best Local Similarity 59.6%; Pred. No. 1e-06;  
Matches 28; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 15 AIWRSNGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTG 61

DB 68 AFWRHNGRNPEKDNFLSRNKENH-KPTSSSLDEKVPASQTTG 113

RESULT 7

Q8NZP4 ID Q8NZP4 PRELIMINARY; PRT; 239 AA.  
AC Q8NZP4;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Hypothetical phage protein spym18\_1802.  
GN SPYM18\_1802.  
OS Streptococcus pyogenes (serotype M18).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=186103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MGAS8232 / Serotype M18;  
RX MEDLINE=21927593; PubMed=11917108;  
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,  
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,  
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
RA Kapur V., Daly J.A., Veasey L.G., Musser J.M.;  
RT "Genome sequence and comparative microarray analysis of serotype M18  
RT group A Streptococcus strains associated with acute rheumatic fever  
RT outbreaks.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
DR EMBL; AE010087; AAL98325.1; --  
DR GO; GO:0003677; F.DNA binding; IEA.  
DR InterPro; IPR005039; Anti\_rep.  
DR Pfam; PF03374; ANT; 1.  
DR Complete proteome; Hypothetical protein.  
KW SEQUENCE 239 AA; 27449 MW; 91988787A84A9853 CRC64;  
SQ SEQUENCE 239 AA; 27449 MW; 91988787A84A9853 CRC64;

Query Match 17.3%; Score 80; DB 16; Length 239;  
Best Local Similarity 29.7%; Pred. No. 1.5;  
Matches 19; Conservative 11; Mismatches 14; Indels 20; Gaps 2;

QY 20 NGSNTL-----ENGYFLSRNKENHSQPTQSSLE-----DSVTPTKAVKT 59

DB 162 NIGQNLFAWLRENGFLIRKNGESYNNFTORSMDMKLFEVKERTHQEPNGSIRISKTKM 221

QY 60 TGKG 63

DB 222 TGRG 225

RESULT 8

Q938N5 ID Q938N5 PRELIMINARY; PRT; 242 AA.  
AC Q938N5;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Antirepressor (Putative P1-type antirepressor-phage associated).  
GN SPYM3\_1261 OR SP50602.  
OS Streptococcus pyogenes, and  
OS Streptococcus pyogenes (serotype M3).

```
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX Streptococcus.
RN NCBI_TaxID=1314, 198466;
RC SEQUENCE FROM N.A.
RA SPECIES=S.pyogenes; STRAIN=NIH1;
RA Ikeda T., Wada A., Inagaki Y., Sugama K., Tanaka D., Suzuki R.,
RA Katsukawa C., Fujinaga Y., Abe Y., Watanabe H.;
RT "Complete sequence of temperate phage PhiNH1.1.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RA SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mamarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RN [3]
RC SEQUENCE FROM N.A.
RA SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, Sf370 and MGAS232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY050245; AAL15047.1; -
DR EMBL; AE014160; AAM79868.1; -
DR EMBL; AP005143; BAC63697.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 242 AA; 27843 MW; 5AA85551447E366C CRC64;

Query Match 17.3%; Score 80; DB 16; Length 242;
Best Local Similarity 35.9%; Pred. No. 1.5;
Matches 23; Conservative 5; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTKAV-KT 59
Db 163 NIGQNKLFQWLRNGYLLSRGSGWNPQTQKSMQLGLFELKKTAINHSDGHTTNTVTKV 222

QY 60 TGKG 63
Db 223 TGKG 226

RESULT 9
O48391 PRELIMINARY; PRT; 238 AA.
AC O48391;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P1-antirepressor homolog.
OS Streptococcus thermophilus bacteriophage TP-J34.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=73422;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=TP-J34;
RX MEDLINE=98122991; PubMed=9454717;
RA Neve H., Zenz K.I., Desiere F., Koch A., Heller K.J., Brussow H.;
RT "Comparison of the lysogeny modules from the temperate streptococcus
RT thermophilus bacteriophages TP-J34 and sf121: implications for the
RT modular theory of phage evolution.";
RL Virology 241:61-72 (1998).

Query Match 16.7%; Score 77; DB 9; Length 287;
Best Local Similarity 34.4%; Pred. No. 3.9;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 208 NIGRKNLFQWLRNGYLLSRGSGWNPQTQKSMQLGLFELKKTININHADGHTTNTTKV 267

QY 60 TGKG 63
Db 268 TGKG 271

RESULT 11
Q8S2U4
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DR EMBL; AF020798; AAC03459.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
SQ SEQUENCE 238 AA; 27081 MW; C30F3E97018EE651 CRC64;

Query Match 16.9%; Score 78; DB 9; Length 238;
Best Local Similarity 34.4%; Pred. No. 2.4;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 159 NIGQNKLFQWLRNGYLLSRGSGWNPQTQKSMQLGLFELKKTININHADGHTTNTTKV 218

QY 60 TGKG 63
Db 219 TGKG 222

RESULT 10
Q38585 PRELIMINARY; PRT; 287 AA.
AC Q38585;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ANTI-repressor protein.
GN ANTI.
OS Streptococcus thermophilus bacteriophage Sfi21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=64186;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=96204576; PubMed=8623559;
RA Bruttin A., Brussow H.;
RT "Site-specific spontaneous deletions in three genome regions of a
RT temperate Streptococcus thermophilus phage.";
RL Virology 219:96-104 (1996).
RN [2]
RC SEQUENCE FROM N.A.
RX MEDLINE=98160788; PubMed=949809;
RA Desiere F., Lucchini S., Bruttin A., Brussow H.;
RT "Evolution of Streptococcus thermophilus bacteriophage genomes by
RT modular exchanges followed by point mutations and small deletions and
RT insertions.";
RL Virology 241:345-356 (1998).
RN [3]
RC SEQUENCE FROM N.A.
RA Desiere F., Lucchini S., Bruttin A., Brussow H.;
RT "Streptococcus thermophilus bacteriophage Sfi21 complete genome.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95646; CAA64937.1; -.
DR EMBL; AF115103; AAD44100.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR005039; Anti_rep.
DR Pfam; PF03374; Anti; 1.
SQ SEQUENCE 287 AA; 33148 MW; 49651DA8F986CF50 CRC64;

Query Match 16.7%; Score 77; DB 9; Length 287;
Best Local Similarity 34.4%; Pred. No. 3.9;
Matches 22; Conservative 6; Mismatches 16; Indels 20; Gaps 3;

QY 20 NSGSNTL-----ENGYFLSRNKENHSOPTQSSLE-----DSVTPTK-AVKT 59
Db 208 NIGRKNLFQWLRNGYLLSRGSGWNPQTQKSMQLGLFELKKTININHADGHTTNTTKV 267

QY 60 TGKG 63
Db 268 TGKG 271

RESULT 11
Q8S2U4
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RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapat G.,  
RA Madueno E., Malcounam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schluter T., Smoes N., Tierrez A.,  
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,  
RA "Comparative genomics of *Listeria* species.",  
RL Science 294:849-852(2001).  
RA EMBL: AL596172; CAC97645.1; -  
DR PIR: AE1734; AE1734.  
DR Lstlist; LINC2418; -  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR005039; Anti rep.  
DR InterPro: IPR003497; BRO\_Nterm.  
DR Pfam: PF01374; ANT; 1.  
DR Pfam: PF02498; Bro-N; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 256 AA; 29082 MW; 5FE3FCEFC81A8B6 CRC64;  
Query Match 15.2%; Score 70; DB 16; Length 256;  
Best Local Similarity 31.4%; Pseq. No. 20;  
Matches 16; Conservative 8; Mismatches 13; Indels 14; Gaps 1;  
QY 27 ENGFFSRNKHNSQPTSSLESVPTK-----AVKTKGK 63  
Db 190 QNGYLISRRTDYNRPQKSMELGLFKIKETAINRSSGAHTAKVTGK 240  
RESULT 15  
Q9VG84  
ID Q9VG84 PRELIMINARY; PRT; 661 AA.  
AC Q9VG84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE CG17227 protein (EC 6.5.1.1) (DNA ligase) (Polydeoxyribonucleotide  
DE synthase [ATP]).  
GN CG17227.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkely;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Aghayani A., An H.-U., Andrews-Franckoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny L., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,  
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferrera S., Frise E., Galie R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of *Drosophila melanogaster* genome.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Flybase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + (DEOXYRIBONUCLEOTIDE)(N) +  
CC {DEOXYRIBONUCLEOTIDE}(M) = AMP + DIPHOSPHATE +  
CC {DEOXYRIBONUCLEOTIDE}(N+M).  
CC -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY.  
DR EMBL: AB003695; AAF54801.2; -  
DR Flybase; FBgn0038035; CG17227.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0003910; F:DNA ligase (ATP) activity; IEA.  
DR GO: GO:0014874; F:ligase activity; IEA.  
DR GO: GO:0006310; P:DNA recombination; IEA.  
DR GO: GO:0006281; P:DNA repair; IEA.  
DR GO: GO:0006260; P:DNA replication; IEA.  
DR InterPro: IPR000977; DNA ligase.  
DR Pfam: PF01068; DNA ligase; 1.  
DR Pfam: PF04579; DNA\_ligase\_A\_C; 1.  
DR Pfam: PF04579; DNA\_ligase\_A\_N; 1.  
DR TIGRfams; TIGR00574; dnll; 1.  
DR PROSITE; PS00697; DNA\_LIGASE\_A1; 1.  
DR PROSITE; PS00333; DNA\_LIGASE\_A2; 1.  
DR PROSITE; PS0160; DNA\_LIGASE\_A3; 1.  
KW ATP-binding; DNA recombination; DNA repair; DNA replication; Ligase.  
SQ SEQUENCE 661 AA; 73899 MW; 5C571C0AF2D7F27 CRC64;

Query Match

15.2%; Score 70; DB 5; Length 661;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 31, 2004, 12:07:20 ; Search time 54 Seconds  
(without alignments)  
470.913 Million cell updates/sec

Title: US-09-989-293A-377  
Perfect score: 462  
Sequence: 1 MTFFLSLLLLVCEAIWRSN.....DSRGLILGAENGWGKVKNT 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	90	3 AAY66748	Aay66748 Membrane-
2	462	100.0	90	3 AAB33469	Aab33469 Human PRO
3	462	100.0	90	4 AAU12408	Aau12408 Human PRO
4	462	100.0	90	4 AAB50922	Aab50922 Human PRO
5	462	100.0	90	4 AAB55271	Aab55271 Human PRO
6	462	100.0	90	6 ABUS8086	Abus8086 Human PRO
7	462	100.0	90	6 ABUS9164	Abus9164 Novel hum
8	462	100.0	90	6 ABUS2676	Abus2676 Human sec
9	462	100.0	90	6 ABO17852	Abol7852 Novel hum
10	462	100.0	90	6 ABUS6059	Abu6059 Human sec
11	462	100.0	90	6 ABU13977	Abu13977 Human PRO
12	462	100.0	90	6 ABUS9116	Abu9116 Human PRO
13	462	100.0	90	6 ABU72562	Abu72562 Novel hum
14	462	100.0	90	6 ABUS6806	Abus6806 Human PRO
15	462	100.0	90	6 ABUS9887	Abus9887 Novel sec
16	462	100.0	90	6 ABUS9311	Abus9311 Human sec
17	462	100.0	90	6 ABO26008	Abol26008 Human PRO
18	462	100.0	90	6 ABO25077	Abol25077 Human PRO
19	462	100.0	90	6 ABUS9017	Abus9017 Human sec
20	462	100.0	90	6 ABUS92395	Abus92395 Novel hum
21	462	100.0	90	6 ABUS9460	Abus9460 Novel hum
22	462	100.0	90	6 ABUS7082	Abus7082 Human sec
23	462	100.0	90	6 ABUS92226	Abus92226 Novel hum
24	462	100.0	90	6 ABU10932	Abu10932 Human PRO
25	462	100.0	90	6 ABUS1684	Abus1684 Novel hum

## ALIGNMENTS

### RESULT 1

AAI66748  
ID AAY66748 standard; protein; 90 AA.

XX AC

XX AAY66748;

DT 05-APR-2000 (first entry)

XX

DE Membrane-bound protein PRO1159.

XX

KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX OS Homo sapiens.

XX

PN WO9963088-A2.

XX

PD 09-DEC-1999.

XX

PF 02-JUN-1999; 99WO-US012252.

XX

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088730P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088741P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

26	462	100.0	90	6 ABUS8623	Abus8623 Human sec
27	462	100.0	90	6 ABO34137	Abol34137 Human PRO
28	462	100.0	90	6 ADA45993	Ada45993 Novel hum
29	462	100.0	90	6 ADA76424	Ada76424 Human PRO
30	462	100.0	90	6 ADA19074	Ada19074 Human PRO
31	462	100.0	90	6 ADA61697	Ada61697 Homo sapi
32	462	100.0	90	6 ADB19482	Adb19482 Novel hum
33	462	100.0	90	6 ADB28023	Adb28023 Human PRO
34	462	100.0	90	6 ADA86502	Ada86502 Novel hum
35	462	100.0	90	6 ADB16066	Adb16066 Human PRO
36	462	100.0	90	6 ADA37888	Ada37888 Human sec
37	462	100.0	90	6 ADA47852	Ada47852 Human PRO
38	462	100.0	90	6 ADA21574	Ada21574 Human sec
39	462	100.0	90	6 ADA10361	Ada10361 Human PRO
40	462	100.0	90	6 ADA67647	Ada67647 Human PRO
41	462	100.0	90	6 ADB30654	Adb30654 Human PRO
42	462	100.0	90	6 ADA85950	Ada85950 Novel hum
43	462	100.0	90	6 ADA17905	Ada17905 Human PRO
44	462	100.0	90	6 ADA97162	Ada97162 Human PRO
45	462	100.0	90	6 ADA79466	Ada79466 Human PRO

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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
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PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
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PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
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PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094551P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
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PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
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PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.

( GETH ) GENENTECH INC.
PA
XX
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WF, Yuan J;
XX
WPI: 2000-072883/06.
N-PSDB; AAZ65094.
DR
DR
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 12; Fig 272; 822pp; English.
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LBL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 90 AA;
Query Match 100.0%; Score 462; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQFTQSSLEDSTVPTKAVKTT 60
DB 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQFTQSSLEDSTVPTKAVKTT 60
```

QY 61 GKGIKGRNLDGRGLILGAEAWGRGVKNT 90  
 Db 61 GKGIKGRNLDGRGLILGAEAWGRGVKNT 90

RESULT 2  
 AAB33469  
 ID AAB33469 standard; protein; 90 AA.  
 AC AAB33469;  
 XX  
 DT 29-JAN-2001 (first entry)  
 XX  
 DE Human PRO1159 protein UNQ589 SEQ ID NO:273.  
 XX  
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;  
 KW haemostatic; antithyroid; antidiabetic; neuroprotective;  
 KW antianaemic; hepatotropic; viricide; antipsoziatic; antiallergic;  
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
 KW osteoarthritis; spondyloarthropathy; Sjogren's syndrome; sarcoidosis;  
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
 KW autoimmune thrombocytopenia; immune-mediated renal disease;  
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
 KW inflammatory bowel disease; gluten-sensitive enteropathy;  
 KW autoimmune disease; immune-mediated skin disease; allergic disease;  
 KW immunological disease; transplantation associated disease;  
 KW graft rejection; graft-versus-host-disease;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200053758-A2.  
 XX  
 PD 14-SEP-2000.  
 XX  
 PF 02-MAR-2000; 2000WO-US005841.  
 XX  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99US-0123618P.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 23-MAR-1999; 99US-0125775P.  
 PR 12-APR-1999; 99US-0128849P.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 28-APR-1999; 99US-0131445P.  
 PR 04-MAY-1999; 99US-0132371P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 28-JUL-1999; 99US-0146222P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020944.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-OCT-1999; 99US-0162508P.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030099.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX  
 DR WPI: 2000-572271/53.  
 DR N-PSDB; AAC58634.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.  
 XX  
 PS Claim 33; Fig 112; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central and  
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel  
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune  
 CC or immune-mediated skin diseases, allergic diseases, immunological  
 CC diseases of the lung, and transplantation associated diseases including  
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578  
 CC represent PCR primers and hybridisation probes used in the isolation of  
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477  
 CC represent human PRO polynucleotide and protein sequences given in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 462; DB 3; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTFFLSLLLLLVCEAIWRSNCSNTLENGYFLSRKNHNSOPTQSSLEDVTPTKAVKTT 60  
 Db 1 MTFFLSLLLLLVCEAIWRSNCSNTLENGYFLSRKNHNSOPTQSSLEDVTPTKAVKTT 60  
 QY 61 KGKIVKGRNLDGRGLILGAEAWGRGVKNT 90  
 Db 61 KGKIVKGRNLDGRGLILGAEAWGRGVKNT 90

RESULT 3  
 AAU12408  
 ID AAU12408 standard; protein; 90 AA.  
 AC AAU12408;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO1159 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
 KW A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200140466-A2.  
XX 07-JUN-2001.  
PD 01-DEC-2000; 2000WO-US032678.  
XX 01-DEC-1999; 99WO-US028301.  
PI 01-DEC-1999; 99WO-US028634.  
PI 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028564.  
XX 02-DEC-1999; 99WO-US028565.  
XX 02-DEC-1999; 99US-0170262P.  
XX 16-DEC-1999; 99WO-US030095.  
XX 20-DEC-1999; 99WO-US030911.  
XX 20-DEC-1999; 99WO-US030999.  
XX 30-DEC-1999; 99WO-US031243.  
XX 30-DEC-1999; 99WO-US031274.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000277.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 24-FEB-2000; 2000WO-US004914.  
XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.  
XX 03-MAR-2000; 2000US-0187202P.  
XX 10-MAR-2000; 2000WO-US006319.  
XX 15-MAR-2000; 2000WO-US006884.  
XX 20-MAR-2000; 2000WO-US007377.  
XX 21-MAR-2000; 2000WO-US007532.  
XX 30-MAR-2000; 2000WO-US008439.  
XX 17-MAY-2000; 2000WO-US013705.  
XX 22-MAY-2000; 2000WO-US014042.  
XX 30-MAY-2000; 2000WO-US014941.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 05-JUN-2000; 2000US-0209832P.  
XX 28-JUL-2000; 2000WO-US020710.  
XX 11-AUG-2000; 2000WO-US022031.  
XX 23-AUG-2000; 2000WO-US023522.  
XX 24-AUG-2000; 2000WO-US023328.  
XX 08-NOV-2000; 2000WO-US030952.  
XX 10-NOV-2000; 2000WO-US030873.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX N-PSDB; AAS21480.  
XX WFI; 2001-408281/43.  
XX N-PSDB; AAS21480.  
XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.  
XX Claim 12; Fig 474; 813pp; English.  
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the

CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy  
XX Sequence 90 AA;  
XX Query Match 100.0%; Score 462; DB 4; Length 90;  
XX Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
XX Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKTT 60  
Db 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNKHSQPTQSSLEDSVPTTKAVKTT 60  
QY 61 GKGIVKGRNLSRGLILGAEAWGRGVKKNT 90  
Db 61 GKGIVKGRNLSRGLILGAEAWGRGVKKNT 90  
RESULT 4  
AAB50922  
ID AAB50922 standard; protein; 90 AA.  
XX AC AAB50922;  
XX 21-MAR-2001 (first entry)  
XX Human PRO1159 protein.  
KW Human; PRO; antiinflammatory; dermatological; antiarthritic;  
KW antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;  
KW antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;  
KW antiallergic; antiasthmatic; immune related disorder;  
KW hepatobiliary disease; autoimmune disease; allergy.  
XX Homo sapiens.  
XX WC200073452-A2.  
XX 07-DEC-2000.  
XX 02-JUN-2000; 2000WO-US015264.  
XX 02-JUN-1999; 99WO-US012252.  
XX 20-JUL-1999; 99US-0144732P.  
XX 20-JUL-1999; 99US-0144759P.  
XX 28-JUL-1999; 99US-0146222P.  
XX 01-SEP-1999; 99WO-US020111.  
XX 15-SEP-1999; 99WO-US021090.  
XX 15-SEP-1999; 99WO-US021547.  
XX 29-OCT-1999; 99US-0162506P.  
XX 30-NOV-1999; 99WO-US028313.  
XX 01-DEC-1999; 99WO-US028634.  
XX 02-DEC-1999; 99WO-US028551.  
XX 02-DEC-1999; 99WO-US028565.  
XX 09-DEC-1999; 99US-0170262P.  
XX 20-DEC-1999; 99WO-US030911.  
XX 05-JAN-2000; 2000WO-US000219.  
XX 06-JAN-2000; 2000WO-US000376.  
XX 11-FEB-2000; 2000WO-US003565.  
XX 18-FEB-2000; 2000WO-US004341.  
XX 18-FEB-2000; 2000WO-US004342.  
XX 22-FEB-2000; 2000WO-US004414.  
XX 24-FEB-2000; 2000WO-US004914.  
XX 24-FEB-2000; 2000WO-US005004.  
XX 01-MAR-2000; 2000WO-US005601.  
XX 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ;  
 PI Gurney AL, Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D;  
 PI Watanabe CK, Wood WI;  
 XX  
 DR WPI; 2001-025253/03.  
 DR N-PSDB; AAC91481.  
 XX  
 XX Thirty three nucleic acids encoding PRO polypeptides which are useful in  
 PT the diagnosis and treatment of immune related disorders, e.g. systemic  
 PT lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis  
 PT and diabetes mellitus.  
 XX  
 PS Claim 58; Fig 42; 218pp; English.  
 XX  
 CC The present sequence is one of thirty three novel PRO polypeptides. The  
 CC PRO polypeptides, anti-PRO antibodies, agonists and antagonists are  
 CC useful for treating and diagnosing immune related disorders such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 CC juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis,  
 CC idiopathic inflammatory myopathies, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, demyelinating diseases of the central and peripheral nervous  
 CC systems (such as multiple sclerosis, idiopathic demyelinating  
 CC demyelinating polyneuropathy), Guillain-Barre syndrome, and chronic inflammatory  
 CC infectious, autoimmune chronic active hepatitis, primary biliary  
 CC cirrhosis, granulomatous hepatitis and sclerosing cholangitis),  
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's  
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous  
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),  
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,  
 CC food hypersensitivity and urticaria), immunological diseases of the lung  
 CC (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and  
 CC hypersensitivity pneumonitis), transplantation associated diseases  
 CC including graft rejection and graft-versus-host diseases  
 XX  
 XX Sequence 90 AA;  
 Query Match 100.0%; Score 462; DB 4; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTFFLSLLLLVCEAIWRNSGNTLNGVFLSRNKENHSQPTQSSLEDVPTKAVKTT 60  
 DB 1 MTFFLSLLLLVCEAIWRNSGNTLNGVFLSRNKENHSQPTQSSLEDVPTKAVKTT 60  
 QY 61 GKGIVKGRNLDGRGLLGAEGWGRGVKKNT 90  
 DB 61 GKGIVKGRNLDGRGLLGAEGWGRGVKKNT 90  
 RESULT 5  
 AAB65271  
 ID AAB65271 standard; protein; 90 AA.  
 AC AAB65271;  
 XX  
 DT 02-APR-2001 (first entry)  
 XX  
 DE Human PRO1159 (UNQ589) protein sequence SEQ ID NO:377.  
 XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
 KW

KW cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 OS Homo sapiens.  
 XX WO200073454-A1.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX  
 XX 02-JUN-1999; 99WO-US012252.  
 XX 23-JUN-1999; 99US-0141037P.  
 XX 07-JUL-1999; 99US-0143048P.  
 XX 20-JUL-1999; 99US-0144758P.  
 XX 26-JUL-1999; 99US-0145698P.  
 XX 28-JUL-1999; 99US-0146222P.  
 XX 17-AUG-1999; 99US-0149396P.  
 XX 15-SEP-1999; 99WO-US021090.  
 XX 15-SEP-1999; 99WO-US021547.  
 XX 08-OCT-1999; 99US-0158663P.  
 XX 30-NOV-1999; 99WO-US028313.  
 XX 01-DEC-1999; 99WO-US028301.  
 XX 16-DEC-1999; 99WO-US030095.  
 XX 20-DEC-1999; 99WO-US030911.  
 XX 05-JAN-2000; 2000WO-US000219.  
 XX 06-JAN-2000; 2000WO-US000376.  
 XX 11-FEB-2000; 2000WO-US003565.  
 XX 18-FEB-2000; 2000WO-US004341.  
 XX 22-FEB-2000; 2000WO-US004414.  
 XX 24-FEB-2000; 2000WO-US004914.  
 XX 24-FEB-2000; 2000WO-US005004.  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX 20-MAR-2000; 2000WO-US007377.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 XX Zhang Z;  
 XX WPI; 2001-032160/04.  
 XX N-PSDB; AAF44240.  
 XX  
 XX PRO polynucleotides used to produce polypeptides used to target bioactive  
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,  
 PT to cause targeted cell death.  
 XX  
 XX Claim 12; Fig 272; 935pp; English.  
 PS  
 XX The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
 CC be used for targeted delivery of bioactive molecules, such as toxins,  
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and  
 CC DNA. They may also be used to produce transgenic animals which are used  
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide  
 CC and protein sequence can be used for tissue typing and in treating  
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
 CC AAF4470 represent PCR primers and hybridisation probes used in the  
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
 CC AAB65300 represent human PRO polynucleotide and protein sequences given  
 CC in the exemplification of the present invention  
 XX  
 XX Sequence 90 AA;  
 Query Match 100.0%; Score 462; DB 4; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy	1	MTFFLSLLILVCAIWRSSGSSNTLNGYFLSRKNKHSGPTOSSLEDVTPTKAVKTT	60
Dd	1	MTFFLSLLILVCAIWRSSGSSNTLNGYFLSRKNKHSGPTOSSLEDVTPTKAVKTT	60
Qy	61	GKGIVKGRNLDRLGILGAEAWGRGVKKNT	90
Dd	61	GKGIVKGRNLDRLGILGAEAWGRGVKKNT	90
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ABUS8086			
ID	ABUS8086	standard; protein; 90 AA.	
XX	ABUS8086;		
AC			
XX			
DT	14-APR-2003	(first entry)	
XX			
DE	Human PRO polypeptide #118.		
XX			
KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;		
KW	horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;		
KW	antibody-dependent enzyme mediated prodrug therapy.		
XX			
OS	Homo sapiens.		
XX			
FN	US2003027163-A1.		
XX			
PD	06-FEB-2003.		
XX			
PF	15-NOV-2001; 2001US-00997666.		
XX			
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PR	17-OCT-1997;	97US-0062250P.	
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PR	12-NOV-1997;	97US-0065186P.	
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PR	24-NOV-1997;	97US-0066770P.	
PR	25-FEB-1998;	98US-0075945P.	
PR	20-MAR-1998;	98US-0078910P.	
PR	28-APR-1998;	98US-0083322P.	
PR	07-MAY-1998;	98US-0084600P.	
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PR	04-JUN-1998;	98US-0088026P.	
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PR	09-JUN-1998;	98US-0088655P.	
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PR	10-JUN-1998;	98US-0088810P.	
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PR	11-JUN-1998;	98US-0088861P.	
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PR	12-JUN-1998;	98US-0089105P.	
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PR	16-JUN-1998;	98US-0089512P.	
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PR	22-JUN-1998;	98US-0090246P.	
PR	22-JUN-1998;	98US-0090252P.	
PR	22-JUN-1998;	98US-0090254P.	
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PR	24-JUN-1998;	98US-0090435P.	
PR	24-JUN-1998;	98US-0090444P.	
PR	24-JUN-1998;	98US-0090445P.	

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PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
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PR 26-AUG-1998; 98US-0097971P.
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PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098252P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-02303978P.

Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTFPLSLLLLYCEATWRSNGSNTLENGYFLSRKNENHSQPTQSSLEDSVPTKAVKTT 60
QY 61 GKGIYKGRNLDGRGLILGAEAWGRGVKNT 90
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Db 61 GKGIYKGRNLDGRGLILGAEAWGRGVKNT 90
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RESULT 7
ABU59164
ID ABU59164 standard; protein; 90 AA.
XX
AC ABU59164;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO1159.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088328P.
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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
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PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
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PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
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PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 98WO-US005028.  
PR 02-JUN-1999; 98WO-US012252.  
PR 15-SEP-1999; 98WO-US021090.  
PR 15-SEP-1999; 98WO-US021547.  
PR 30-NOV-1999; 98WO-US028313.  
PR 01-DEC-1999; 98WO-US028301.  
PR 01-DEC-1999; 98WO-US028634.  
PR 16-DEC-1999; 98WO-US030095.  
PR 20-DEC-1999; 98WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000WO-US023328.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Borstein D, Desnoyers L, Eaton DL;  
XX PI Ferrara N, Fong S, Gerber H, Gerecht ME, Goddard A, Godowski PJ;  
XX PI Grimaldi JC, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF;  
XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
XX PI Zhang Z;  
XX  
XX WPI; 2003-247083/24.  
XX N-PSDB; ABX80363.  
XX  
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
XX PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
XX PT are therapeutically useful for enhancing immune response and in cancer  
XX PT treatments.

PS Claim 12; Fig 272; 648pp; English.  
XX  
CC The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth. and PRO536,  
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813  
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein  
XX  
SQ Sequence 90 AA;  
Query Match 100.0%; Score 462; DB 6; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVPTKAVKTT 60  
Db 1 MTFFLSLLLLVCEAIWRSNGSNTLENGYFLSRKNHNSQPTQSSLEDSVPTKAVKTT 60  
QY 61 GKGIVKGRNLDGRGLILGAEAWGRGVKNT 90  
Db 61 GKGIVKGRNLDGRGLILGAEAWGRGVKNT 90  
RESULT 8  
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ID ABU82676 standard; protein; 90 AA.  
XX  
XX AC ABU82676;  
XX  
XX DT 26-JUN-2003 (first entry)  
XX  
XX DE Human secreted/transmembrane protein PRO1159.  
XX  
XX KW Human; PRO; secreted protein; transmembrane protein;  
XX KW cardiac insufficiency disorders; angiogenesis; wound healing;  
XX KW cancerous tumour; immune response; retinal disorder; sight loss;  
XX KW retinitis pigmentosum; age-related macular degeneration; AMD;  
XX KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;  
XX KW Crohn's disease; sports injury; arthritis.  
OS  
XX Homo sapiens.  
XX  
XX US2003032023-A1.  
XX  
XX PD 13-FEB-2003.  
XX  
XX PF 14-NOV-2001; 2001US-00990711.  
XX  
XX PF 16-JUN-1997; 97US-0049787P.



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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
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PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFLLSLLLIVCEAIWRSNGSNTLENGYFLSRKNENHSQTSOLESLSVTPKAVKTT 60
Db 1 MTFLLSLLLIVCEAIWRSNGSNTLENGYFLSRKNENHSQTSOLESLSVTPKAVKTT 60

QY 61 GKGIVKGRNLDRLGLILCAEAWGRGVKNT 90
Db 61 GKGIVKGRNLDRLGLILCAEAWGRGVKNT 90

RESULT 9
AB017852
ID AB017852 standard; protein; 90 AA.
XX
AC AB017852;
XX
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1159.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antididiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
FN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-0014047A.
XX
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PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022931.
PR 29-OCT-1998; 98WO-US022932.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005130.
PR 20-APR-1999; 99WO-US006615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021030.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 05-JAN-2000; 2000WO-US031274.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 01-MAR-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 10-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
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01-MAR-2001; 2001WO-US006666.  
09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI: 2003-341980/32.  
DR N-PSDB; ACD24089.  
XX  
XX New secreted and transmembrane PRO nucleic acids, for treating  
PT inflammation, organ failure, atherosclerosis, cardiac injury,  
PT infertility, birth defects, premature aging, acquired immunodeficiency  
PT syndrome (AIDS), or cancer.  
XX  
PS Claim 12; Fig 474; 660pp; English.  
XX  
CC The invention describes an isolated nucleic acid (I) comprising, or which  
CC has 80 % sequence identity to, or the full-length coding sequence of, one  
CC of 275 nucleotide sequences, and which encodes a corresponding  
CC polypeptide selected from 275 amino acid sequences, where all sequences  
CC are given in the specification. The polypeptide encoded by (I) is used to  
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
CC the proliferation or differentiation of cells or gene expression,  
CC stimulate the release of proteoglycans, stimulate the release of cytokine  
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
CC acid and polypeptide encoded by it, are useful for treating inflammatory  
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
CC birth defects, premature aging, acquired immunodeficiency syndrome  
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
CC hybridisation probes, in chromosome and gene mapping, and in generating  
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This is the amino acid sequence of a novel human secreted and  
CC transmembrane PRO polypeptide  
XX  
SQ Sequence 90 AA;

Query Match 100.0%; Score 462; DB 6; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSQPTQSSLESVTPTKAVKTT 60

Db 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRKNKHSQPTQSSLESVTPTKAVKTT 60  
QY 61 GKGIKGRNLDNRGLILGAEAWGRGVKNT 90  
Db 61 GKGIKGRNLDNRGLILGAEAWGRGVKNT 90  
RESULT 10  
ABU60595  
ID ABU60595 standard; protein; 90 AA.  
AC ABU60595;  
XX  
DT 01-MAY-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein, #154.  
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
diagnostic; therapeutic; gene therapy.  
XX Homo sapiens.  
XX US2002160384-A1.  
XX 31-OCT-2002.  
XX  
PF 14-NOV-2001; 2001US-00992598.  
XX  
PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Borstein D, Deanovsers L, Eaton DL,  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini IO, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
PI Zhang Z;  
XX  
XX WPI; 2003-288106/28.  
DR N-PSDB; ABX90341.  
XX  
PT New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes.  
XX  
XX Claim 12; Fig 272; 650pp; English.  
PS  
CC The invention discloses isolated PRO secreted/transmembrane polypeptides  
CC comprising a sequence without signal peptide and the nucleic acid  
CC encoding them. The polypeptides can be used to raise antibodies that  
CC specifically bind to the PRO polypeptide, for linking a bioactive  
CC molecule to a cell expressing a PRO protein and for modulating at least  
CC one biological activity of a cell. The PRO polypeptides or

CC polynucleotides are also useful in gene therapy, in chromosome  
CC identification, as chromosome markers, or in generating probes. The PRO  
CC polypeptides are useful as molecular markers for protein electrophoresis,  
CC and the isolated nucleic acids may be used for recombinantly expressing  
CC those markers. The PRO polypeptides and nucleic acids may also be used in  
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for  
CC PRO, and in affinity purification of PRO from recombinant cell culture or  
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC is also available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 90 AA;  
Query Match 100.0%; Score 462; DB 6; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTFLLSLLLLVCEAIWRSNLSGNTLENGYFLSRKNHNSQPTSSLSDSVTPTKAVKTT 60  
Db 1 MTFLLSLLLLVCEAIWRSNLSGNTLENGYFLSRKNHNSQPTSSLSDSVTPTKAVKTT 60  
QY 61 KGKIVKGNLDSRGLILGAEAWGRGVKNT 90  
Db 61 KGKIVKGNLDSRGLILGAEAWGRGVKNT 90  
RESULT 11  
ABU13977  
ID ABU13977 standard; protein; 90 AA.  
XX  
XX ABU13977;  
XX  
XX 26-FEB-2003 (first entry)  
XX  
XX Human PRO1159 polypeptide.  
XX  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive.  
XX  
XX Homo sapiens.  
XX  
XX US2002103125-A1.  
XX  
XX 01-AUG-2002.  
XX  
XX 20-NOV-2001; 2001US-00989731.  
XX  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-US020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0068770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
XX 28-MAY-1998; 98US-0087106P.  
XX 02-JUN-1998; 98US-0087607P.  
XX 02-JUN-1998; 98US-0087609P.  
XX 03-JUN-1998; 98US-0087759P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088025P.  
XX 04-JUN-1998; 98US-0088026P.  
XX 04-JUN-1998; 98US-0088028P.  
XX 04-JUN-1998; 98US-0088029P.  
XX 04-JUN-1998; 98US-0088030P.  
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XX 04-JUN-1998; 98US-0088326P.  
XX 05-JUN-1998; 98US-0088167P.  
XX 05-JUN-1998; 98US-0088202P.





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PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
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PR 17-SEP-1997; 97US-0059122P.
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PR 19-SEP-1997; 97US-0059352P.
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PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0063287P.
PR 17-OCT-1997; 97US-0063755P.
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PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 28-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 11-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073512P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079563P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.

XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood W, Zhang Z;
XX WPI: 2003-352836/33.
DR N-PSDB; ACA67230.
XX
XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX Claim 12; Fig 474; 643pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABUS0870-ABUS1144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdentry.html
XX
SQ Sequence 90 AA;
Query Match 100.0%; Score 462; DB 6; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.8e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTFELSLLLLVCEAIWRSNSGNTLENGYFLSRKNHNSOPTQSSLSDSVTPTKAVKTT 60
Db 1 MTFELSLLLLVCEAIWRSNSGNTLENGYFLSRKNHNSOPTQSSLSDSVTPTKAVKTT 60
QY 61 GKGIYKGRNLDGRGLILGAEAWGRGVKXNT 90
Db 61 GKGIYKGRNLDGRGLILGAEAWGRGVKXNT 90
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RESULT 13  
ABU72562  
ID ABU72562 standard; protein; 90 AA.  
XX AC ABU72562;  
XX DT 17-JUN-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1159.  
XX KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;  
XX KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
XX KW PRO; pharmacological; diagnostic; biosensor; bioreactor; malignancy;  
XX KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
XX KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
XX KW drug screening.  
XX OS Homo sapiens.  
XX PN US2003003531-A1.  
XX PD 02-JAN-2003.  
XX PF 19-NOV-2001; 2001US-00989734.  
XX PR 16-JUN-1997; 97US-00497872.  
XX PR 17-OCT-1997; 97US-0062250P.  
XX PR 05-NOV-1997; 97WO-US020069.  
XX PR 12-NOV-1997; 97US-0065186P.  
XX PR 13-NOV-1997; 97US-0065311P.  
XX PR 24-NOV-1997; 97US-0066770P.  
XX PR 25-FEB-1998; 98US-0075945P.  
XX PR 20-MAR-1998; 98US-0078910P.  
XX PR 28-APR-1998; 98US-0083322P.  
XX PR 07-MAY-1998; 98US-0084600P.  
XX PR 28-MAY-1998; 98US-0087106P.  
XX PR 02-JUN-1998; 98US-0087607P.  
XX PR 02-JUN-1998; 98US-0087609P.  
XX PR 02-JUN-1998; 98US-0087759P.  
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XX PR 04-JUN-1998; 98US-0088021P.  
XX PR 04-JUN-1998; 98US-0088025P.  
XX PR 04-JUN-1998; 98US-0088026P.  
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XX PR 04-JUN-1998; 98US-0088033P.  
XX PR 04-JUN-1998; 98US-0088326P.  
XX PR 05-JUN-1998; 98US-0088167P.  
XX PR 05-JUN-1998; 98US-0088202P.  
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XX PR 05-JUN-1998; 98US-0088217P.  
XX PR 09-JUN-1998; 98US-0088655P.  
XX PR 10-JUN-1998; 98US-0088734P.  
XX PR 10-JUN-1998; 98US-0088738P.  
XX PR 10-JUN-1998; 98US-0088742P.  
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XX PR 11-JUN-1998; 98US-0088858P.  
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XX PR 16-JUN-1998; 98US-0089440P.  
XX PR 16-JUN-1998; 98US-0089512P.  
XX PR 16-JUN-1998; 98US-0089514P.  
XX PR 17-JUN-1998; 98US-0089532P.  
XX PR 17-JUN-1998; 98US-0089538P.  
XX PR 17-JUN-1998; 98US-0089598P.  
XX PR 17-JUN-1998; 98US-0089599P.  
XX PR 17-JUN-1998; 98US-0089600P.  
XX PR 17-JUN-1998; 98US-0089653P.  
XX PR 18-JUN-1998; 98US-0089801P.

PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030311.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Grissins ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;  
XX WPI; 2003-352829/33.  
DR N-PSDB; ACA64409.  
XX  
XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
PT disease.  
XX  
XX Claim 12; Fig 272; 663pp; English.  
XX  
CC The invention describes a new isolated nucleic acid molecule comprising  
CC the full length coding sequence of the DNA deposited with the American  
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PFA, 819-PFA,  
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA  
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These  
CC are particularly useful for detecting or treating e.g. malignancies or  
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's

CC disease in mammals. The PRO polypeptides are useful in drug screening,  
CC particularly as targets for therapeutic intervention in these diseases,  
CC and in the diagnostic determination of the presence of these diseases.  
CC The PRO polypeptides are also useful as molecular weight markers, or for  
CC chromosome identification. The PRO genes are useful as hybridisation  
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
CC The PRO genes may also be used in gene therapy, particularly for  
CC replacing a defective gene. This is the amino acid sequence of a novel  
CC human secreted and transmembrane PRO polypeptide

XX Sequence 90 AA;

Query Match 100.0%; Score 462; DB 6; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9,8e-49;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTFFLSLLLLVCEAIWRNSGNTLENGYFLSRKNHNSQPTQSSLEDSVTPTKAVKTT 60  
QY 61 GKGIVKGRNLDGRGLILGAEWGRGVKNT 90  
DB 61 GKGIVKGRNLDGRGLILGAEWGRGVKNT 90

#### RESULT 14

ABU66806  
ID ABU66806 standard; protein; 90 AA.

XX AC ABU66806;

XX 23-MAY-2003 (first entry)

XX Human PRO polypeptide #237.

KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.  
OS Homo sapiens.

PN US2003036180-A1.

XX 20-FEB-2003.

XX 09-MAY-2002; 2002US-00143114.

XX 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022591.

PR 29-OCT-1998; 98WO-US022592.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015284.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 09-MAR-2001; 2001WO-US006666.  
PR 14-MAR-2001; 2001US-00802706.  
PR 22-MAR-2001; 2001US-00808689.  
PR 05-APR-2001; 2001US-00816744.  
PR 10-MAY-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 18-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001US-00872035.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 23-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

XX (GETH ) GENENTECH INC.  
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI; 2003-332040/31.  
 DR N-PSDB; ACA03839.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, useful for gene  
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue  
 PT typing, and in chromosome identification.  
 XX  
 PS Claim 12; Fig 474; 660pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides are useful for detecting other PRO polypeptides, for linking  
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
 CC biological activities of cells expressing PRO polypeptides, and for for  
 CC identifying agonists or antagonists. The PRO polypeptides are useful for  
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from  
 CC human blood, for stimulating the proliferation or differentiation of  
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide  
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,  
 CC in chromosome and gene mapping, in the generation of antisense RNA and  
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic  
 CC animals or knockout animals, for the genetic analysis of individuals with  
 CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the  
 CC human PRO polypeptides of the invention. NOTE: The sequence data for this  
 CC patent was obtained in electronic format directly from the USPTO web site  
 CC at seqdata.uspto.gov/psipdsIDentry.html  
 XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 462; DB 6; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-49;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MTFPLSLLLLVCEAIWRNSGNTLENGYFLSRNKENHSQPTOSLSDSVTPKAVKTT 60  
 QY 61 GKGIVKGRNLDRLGLILGAEWGRGVKNT 90  
 Db 61 GKGIVKGRNLDRLGLILGAEWGRGVKNT 90  
 RESULT 15  
 ABUS9887  
 ID ABUS9887 standard; protein; 90 AA.  
 AC ABUS9887;  
 XX  
 XX 13-MAY-2003 (first entry)  
 DT  
 XX  
 DE Novel secreted and transmembrane protein PRO1159.  
 XX  
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocyte stimulation;  
 KW retinal neurons cell survival; rod photoreceptor cell survival;  
 KW retinal disorder; retinitis pigmentosa; kidney disease;  
 KW mammalian kidney mesangial cell proliferation; Berger disease;  
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
 KW chondrocyte redifferentiation; sports injury; arthritis.  
 XX  
 OS Homo sapiens.  
 XX

PN US2003017563-A1.  
 XX  
 PD 23-JAN-2003.  
 XX  
 PF 07-MAY-2002; 2002US-00140808.  
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 PR 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017888.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 29-OCT-1998; 98WO-US022991.  
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 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99WO-US005190.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 13-SEP-1999; 99WO-US020344.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 05-OCT-1999; 99WO-US021547.  
 PR 23-NOV-1999; 99WO-US023089.  
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 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
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 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
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 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

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588,739 Million cell updates/sec

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- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	462	100.0	90	9	US-09-989-273-377
4	462	100.0	90	9	US-09-989-721-377
5	462	100.0	90	9	US-09-989-731-377
6	462	100.0	90	9	US-09-989-732-377
7	462	100.0	90	9	US-09-991-073-377
8	462	100.0	90	9	US-09-990-442-377
9	462	100.0	90	9	US-09-991-163-377
10	462	100.0	90	9	US-09-993-604-377
11	462	100.0	90	9	US-09-990-456-377
12	462	100.0	90	9	US-09-989-721-377
13	462	100.0	90	9	US-09-992-598-377
14	462	100.0	90	9	US-09-989-293A-377
15	462	100.0	90	9	US-09-989-735-377

16	462	100.0	90	9	US-09-990-444-377
17	462	100.0	90	9	US-09-991-181-377
18	462	100.0	90	9	US-09-989-730-377
19	462	100.0	90	9	US-09-990-436-377
20	462	100.0	90	9	US-09-993-687-377
21	462	100.0	90	10	US-09-989-734-377
22	462	100.0	90	10	US-09-997-653-377
23	462	100.0	90	10	US-09-991-667-377
24	462	100.0	90	10	US-09-997-428-377
25	462	100.0	90	10	US-09-997-666-377
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34	462	100.0	90	10	US-09-997-573-377
35	462	100.0	90	10	US-09-991-172-377
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42	462	100.0	90	10	US-09-997-683-377
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44	462	100.0	90	10	US-09-997-349-377
45	462	100.0	90	10	US-09-997-440-377

## ALIGNMENTS

RESULT 1  
US-09-989-722-377  
; Sequence 377, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P27301C63  
; CURRENT APPLICATION NUMBER: US/09/989,722  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17



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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
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; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Feng, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478

; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091544  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
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; PRIOR APPLICATION NUMBER: 60/091978  
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; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
  
Query Match 100.0%; Score 462; DB 9; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.6e-47;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 3  
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; Sequence 377, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC56  
; CURRENT APPLICATION NUMBER: US/09/989,279  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1997-11-12  
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21	PRIOR APPLICATION NUMBER: 60/088025	21	PRIOR FILING DATE: 1998-06-22
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51	PRIOR APPLICATION NUMBER: 60/088810	51	PRIOR FILING DATE: 1998-06-25
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55	PRIOR APPLICATION NUMBER: 60/088826	55	PRIOR FILING DATE: 1998-06-25
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58	PRIOR FILING DATE: 1998-06-11	58	PRIOR APPLICATION NUMBER: 60/090695
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63	PRIOR APPLICATION NUMBER: 60/089105	63	PRIOR FILING DATE: 1998-06-26
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; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-989-727-377
; Sequence 377, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301065
; TITLE OF INVENTION: Acids Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
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; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC70  
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
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; Patent No. US2002013252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
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; APPLICANT: Williams, P. Mickey  
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; APPLICANT: Zhang, Zemin  
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; FILE REFERENCE: P2730PIC25  
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Query Match      100.0%; Score 462; DB 9; Length 90;
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Qy 61 GKGVKGRNLDNRGLILGAEGWGRGVKNT 90
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## RESULT 12

US-09-989-721-377

; Sequence 377, Application US/099893721

; Patent No. US20020142961A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C55

; CURRENT APPLICATION NUMBER: US/09/989, 721

; CURRENT FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

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52 PRIOR FILING DATE: 1998-07-09

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RESULT 13

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1 Sequence 377, Application US/09992598  
2 Patent No. US20020160384A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Ashkenazi, Avi J.  
5 APPLICANT: Baker, Kevin P.  
6 APPLICANT: Botstein, David  
7 APPLICANT: Desnoyers, Luc  
8 APPLICANT: Eaton, Dan L.  
9 APPLICANT: Ferrara, Napoleone  
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25 APPLICANT: Williams, P. Mickey  
26 APPLICANT: Wood, William I.  
27 APPLICANT: Zhang, Zemin  
28 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
29 FILE REFERENCE: P2730PIC20  
30 CURRENT APPLICATION NUMBER: US/09/992,598  
31 CURRENT FILING DATE: 2001-11-14  
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Query Match 100.0%; Score 462; DB 9; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.6e-47;

Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 377, Application US/09989293A  
; Patent No. US20020177164A1

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTFPLSLLLLVCEAIWRSGNSTLNGYFLSRNKENHSQPTOSSLEDSVTPTKAVKTT 60

Qy 61 GKGIVKGRNLDLSRGLILGAEAWGRGVKNT 90
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; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Forst, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 462; DB 9; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.6e-47; Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTFFLSLLLLVCEAIWRNSGNTLENGVFLSRKNHSGTOSSLEDSVTPKAVKTT 60

Db 1 MTFFLSLLLLVCEAIWRNSGNTLENGVFLSRKNHSGTOSSLEDSVTPKAVKTT 60

Qy 61 KGKIVKGRNLDNRGLILGAENWGRGVKNT 90

Db 61 KGKIVKGRNLDNRGLILGAENWGRGVKNT 90

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Job time : 41 secs